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OM protein - protein search, using sw model

Run on: October 16, 2005, 20:17:32 ; Search time 30 Seconds
(without alignments)
229.173 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155
Sequence: 1 XXHADGFSDEMTXLDLAXXDPINWXXTKITDXX 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 846186 seqs, 185815562 residues

Total number of hits satisfying chosen parameters: 846186

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Pending Patents AA New:*

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OM protein - protein search, using sw model

Run on: October 17, 2005, 12:49:43 ; Search time 150.5 Seconds
(without alignments)
287.151 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155
Sequence: 1 XXHADGSPSDEMTXLDXIXXDFINMLXRTITDXX 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database.: Pandina-Database AA Multi.

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OM protein - protein search, using SW model

Run on: October 17, 2005, 12:49:43 ; Search time 150.5 Seconds
(without alignments)
287.151 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155
Sequence: 1 XXHADGSFSDENWTYLDXLLAXXDFINWIXXTKITDXX 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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OM protein - protein search, using sw model

Run on: October 16, 2005, 20:17:32 ; Search time 30 Seconds
(without alignments)
229.173 Million cell updates/sec

Title: US-10-042-746-2
Perfect score: 174
Sequence: 1 XXHADGSPDEWNTILDLNLAARDFINWLIQTITDXX 37

Scoring table: BIOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 846186 seqs, 185815562 residues

Total number of hits satisfying chosen parameters: 846186

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

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OM protein - protein search, using sw model

Run on: October 17, 2005, 12:49:43 ; Search time 150.5 Seconds
(without alignments)
287.151 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174
Sequence: 1 XHAGDSFSDENATIDNAXRDPINWLTQTKTDIX 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 116806243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 17:15:41 ; Search time 5962.5 Seconds
(without alignments)
253.325 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155
Sequence: 1 XXHADGSPSDENNTYLDYLAAXDFINMLXTKITDXX 37

Scoring table: BLOSUM62DX

Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5
Rgapop 6.0	Rgapext 7.0
Delop 6.0	Delext 7.0

Searched: 4554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Command line parameters:
-MODBL=frame+ p2n.model -DEV=xlh
-O=/cgn2.1/USPTO.spool/US10042746/runat.17102005.100128.4866/app.query.fasta.1
-DB=Pending Patents NA Main -QFMT=fastap -SUFFIX=rpnm -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62dx -TRANS=human40.cdi
-LIST=200 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=125
-MODE=LOCAL -OUTFMT=pcio -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10042746@cgn.1.1.5523 @runat.17102005.100128.4866 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -RGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
Database : Pending Patents NA Main:*

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 16, 2005, 21:05:22 ; Search time 1126 Seconds
(without alignments)
459.127 Million cell updates/sec

Title: US-10-042-746-1
Perfect score: 155
Sequence: 1 XXHADGSPDENNTXLDXLDXDPINWLXXXTKTDXX 37

Scoring table: BIOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2682026 segs, 6986173828 residues

Total number of hits satisfying chosen parameters: 53640412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 200 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US10042746/runac_14102005_180155_4174/app_query_fasta-
-DB=pending_Patents_NA_New -QFMT=fastap -SUFFIX=rnpn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bl0sum62DX -TRANS=human40.cdi
-LIST=200 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=200
-MODE=LOCAL -OUTFMT=pco -NOM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10042746@cgn_1_1_247 @runac_14102005_180155_4174 -NCPU=6 -ICPU=3
-NO MMAP -LARGESQUDERY -NEG_SCORES=0 -WAIT_DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=
-Fgapext=7. -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending_Patents_NA_New:*

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 17:17:30 ; Search time 490 Seconds
(without alignments)
529.404 Million cell updates/sec

Title: US-10-042-746-2
Perfect score: 174
Sequence: 1 XXHADGFSDEMNITLNLAKRDPFNNWLIQTXTDX 37

Scoring table: BLOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 8766186 seqs, 3505510206 residues

Total number of hits satisfying chosen parameters: 17532372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=r1h
-Q=/cgn2.1/USFTO_spool/US10042746/runat_17102005_100128_4884/app_query.fasta_1.3
-DB=published.Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62DX
-TRANS-human40.cdi -LIST=200 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=125 -MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000
-USER=US10042746 @CGC 1.1.582 @runat_17102005_100128_4884 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 16, 2005, 21:05:22 ; Search time 1126 Seconds.
(without alignments)
459.127 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174
Sequence: 1 XXHADGSFSDENMTILDNLAKRDFINWLIQTKITDX 37

Scoring table: BLOSUM62DX

Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 26820206 segs, 6986173828 residues

Total number of hits satisfying chosen parameters: 53640412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DRV=xlh
-O=/cgn2.1/USPTO.spool/US10042746/runat_14102005_180155_4174/app.query.fasta.1
-DB=Pending_Patents_NA_New -OPMT=fastap -SUFFIX=rnpn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62dx -TRANS=human40.cdi
-LIST=200 -DOCALLIGN=200 -THR SCOR=pct -THR MAX=100 -THR MIN=0 -ALIGN=200
-MODE=LOCAL -OUTPMT=pco -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10042746 @CGN 1 1 247 @runat_14102005_180155_4174 -NCPU=6 -ICPU=3
-NO MAP -LARGOQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Tue Oct 18 16:18:23 2005

US-10-042-746-2.rupm

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 17:15:41 ; Search time 5962.5 seconds

Title: US-10-042-746-2 (without alignments)
Perfect score: 174 253.325 Million cell updates/sec

Sequence: 1 XCHADGFSFDEWNTIIDLNLAXRDPINWLTQTKITDX 37

Scoring table: BLOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US10042746/runat_17102005_100128_4866/app.query.fasta.1.3
-DB=Pending Patents NA.Main -QPM=faetap -SUFFIX=rupm -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62dx -TRANS=human40.cdi
-LIST=200 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=125
-MODE=LOCAL -OUTWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10042746.@CGN.1.1.5523@runat_17102005_100128_4866 -NCPU=6 -ICPU=3
-NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
atbase . Database Database NA.Main.1

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 16, 2005, 20:52:27 ; Search time 123.5 Seconds

(without alignments)
490.221 Million cell updates/sec

Title: US-10-042-746-2

Sequence: 1 XHAGSFSDEMTIINDINAXRDFIMWLQTKITDX 37

Scoring table:

BLOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%
Listing first 200 summaries

Command line parameters:

-MODE=frame_p2n.model -DEV=xlh
-Q/cg2_1/USPTO.spool/US10047746/rnuc 14102005 180154 4144/app query.fasta_1.398
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPTL=0
-LOOPEXT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=blomsu62DX -TRANS=human40.ccd
-LIST=200 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=200
-MODE=LOCAL -OUTFMT=ptc -NORMext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10047746 -WCEN 1.93 -runcat 14102005 180154 4144 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-BEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA: *
1: /cg2_6/prodata/1/ina/5A.COMB.seg:*
2: /cg2_6/prodata/1/ina/5B.COMB.seg:*
3: /cg2_6/prodata/1/ina/5A.COMB.seg:*
4: /cg2_6/prodata/1/ina/5B.COMB.seg:*
5: /cg2_6/prodata/1/ina/5A.COMB.seg:*
6: /cg2_6/prodata/1/ina/5B.COMB.seg:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	174	100.0	895	3	US-08-784-582-55
2	174	100.0	955	3	US-08-784-582-55
3	174	100.0	955	3	US-08-784-582-55
4	174	100.0	1062	4	US-09-016-434-1212
5	174	100.0	2356	4	US-08-784-582-72
6	76	43.7	207	1	US-08-193-863-3
7	76	43.7	207	1	US-08-377-833-3
8	76	43.7	207	1	US-08-324-502-3
9	76	43.7	207	1	US-08-083-501-3
10	76	43.7	207	1	US-08-415-939-3
11	74	42.5	144	2	US-08-835-231-17
12	74	42.5	144	3	US-09-108-661-17

13	72	41.4	143	2	US-08-835-231-14	Sequence 14, Appl
14	72	41.4	143	3	US-09-108-661-14	Sequence 14, Appl
15	72	41.4	159	2	US-08-835-231-15	Sequence 15, Appl
16	72	41.4	159	3	US-09-108-661-15	Sequence 15, Appl
17	72	41.4	528	2	US-08-835-231-7	Sequence 7, Appl
18	72	41.4	528	2	US-08-835-231-8	Sequence 8, Appl
19	72	41.4	528	3	US-09-108-661-7	Sequence 7, Appl
20	72	41.4	528	3	US-09-108-661-8	Sequence 8, Appl
21	72	41.4	711	4	US-09-949-016-3581	Sequence 3581, Ap
22	72	41.4	13795	4	US-09-949-016-15323	Sequence 15323, A
23	71	40.8	110	1	US-07-741-931-8	Sequence 8, Appl
24	71	40.8	110	1	US-07-741-931-9	Sequence 9, Appl
25	71	40.8	110	1	US-07-937-132A-8	Sequence 8, Appl
26	71	40.8	110	1	US-07-937-132A-9	Sequence 9, Appl
27	71	40.8	255	4	US-09-280-030-51	Sequence 51, Appl
28	70	40.2	561	2	US-08-835-231-3	Sequence 3, Appl
29	70	40.2	561	2	US-08-835-231-4	Sequence 4, Appl
30	70	40.2	561	3	US-09-108-661-3	Sequence 3, Appl
31	70	40.2	561	3	US-09-108-661-4	Sequence 4, Appl
32	69	39.7	87	1	US-07-741-931-1	Sequence 1, Appl
33	69	39.7	87	1	US-07-741-931-1	Sequence 1, Appl
34	69	39.7	87	4	US-09-280-030-59	Sequence 59, Appl
35	66	37.9	107	1	US-07-741-931-11	Sequence 11, Appl
36	66	37.9	107	1	US-07-937-132A-11	Sequence 11, Appl
37	63	36.2	107	1	US-07-741-931-10	Sequence 10, Appl
38	63	36.2	107	1	US-07-937-132A-10	Sequence 10, Appl
39	59	33.9	492	4	US-09-019-172-1	Sequence 1, Appl
40	58	33.3	138	4	US-09-614-847-146	Sequence 146, App
41	58	33.3	1079	3	US-08-789-328C-6	Sequence 6, Appl
42	58	33.3	1088	3	US-08-789-328C-2	Sequence 2, Appl
43	58	33.3	6529	3	US-08-789-328C-1	Sequence 1, Appl
44	57.5	33.0	1713	4	US-09-489-039A-4371	Sequence 4371, Ap
45	57	32.8	891	4	US-09-540-236-962	Sequence 962, App
46	57	32.8	1477	4	US-09-540-236-962	Sequence 962, App
47	57	32.8	1511	4	US-09-708-392-16	Sequence 16, Appl
48	57	32.8	1511	4	US-09-708-392-18	Sequence 18, Appl
49	57	32.8	1511	4	US-09-949-016-481	Sequence 481, App
50	57	32.8	2538	4	US-09-543-681A-193	Sequence 193, App
51	57	32.8	269223	4	US-09-596-002-41	Sequence 41, Appl
52	56	33.2	129	3	US-08-789-328C-11	Sequence 11, Appl
53	56	33.2	138	3	US-08-789-328C-12	Sequence 12, Appl
54	55	31.6	105	3	US-08-995-366-6	Sequence 6, Appl
55	55	31.6	105	5	PCT-US95-10075-6	Sequence 6, Appl
56	55	31.6	186	4	US-09-489-039A-2085	Sequence 2085, A
57	55	31.6	1866	4	US-09-489-039A-2085	Sequence 2085, Ap
58	55	31.6	580073	4	US-08-545-558D-1	Sequence 1, Appl
59	54.5	31.3	1614	4	US-09-252-991A-10453	Sequence 10453, A
60	54.5	31.3	3255	4	US-09-252-991A-10617	Sequence 10617, A
61	54.5	31.3	3375	4	US-09-252-991A-10239	Sequence 10239, A
62	54	31.0	765	4	US-09-270-767-13413	Sequence 13413, A
63	54	31.0	1314	4	US-09-543-681A-2105	Sequence 2105, Ap
64	54	31.0	3669	4	US-09-774-558-235	Sequence 235, App
65	54	31.0	3784	1	US-07-623-033-1	Sequence 1, Appl
66	54	31.0	4112	4	US-07-799-451-706	Sequence 706, App
67	54	31.0	12860	4	US-09-949-016-12223	Sequence 12223, A
68	54	31.0	12861	4	US-09-949-016-13426	Sequence 13426, A
69	53.5	30.7	3779	3	US-09-221-017B-247	Sequence 247, App
70	53	30.5	954	4	US-09-540-236-1910	Sequence 1910, Ap
71	53	30.5	4358	4	US-09-949-016-4533	Sequence 4533, Ap
72	53	30.5	4359	4	US-09-949-016-725	Sequence 725, App
73	53	30.5	4869	4	US-09-949-016-17507	Sequence 17507, A
74	53	30.5	31940	4	US-09-556-002-13	Sequence 13, Appl
75	52.5	30.2	344	4	US-09-270-767-1364	Sequence 1364, Ap
76	52.5	30.2	344	4	US-09-270-767-16646	Sequence 16646, Ap
77	52	29.9	320	4	US-09-513-999C-27903	Sequence 27903, A
78	52	29.9	366	3	US-08-908-643C-54	Sequence 54, Appl
79	52	29.9	426	3	US-08-908-643C-52	Sequence 52, Appl
80	52	29.9	498	3	US-08-908-643C-50	Sequence 50, Appl
81	52	29.9	882	1	US-08-628-291-3	Sequence 3, Appl
82	52	29.9	882	2	US-09-128-722-3	Sequence 3, Appl
83	52	29.9	914	4	US-09-270-767-9986	Sequence 9986, Ap
84	52	29.9	1204	1	US-08-638-291-11	Sequence 11, Appl
85	52	29.9	1204	2	US-09-128-722-11	Sequence 11, Appl

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 17:10:34 ; Search time 373.5 Seconds

(without alignments)
586,427 Million cell updates/sec

Title: US-10-042-746-2
Sequence: 1 XHHADGSPDEMTLIDNLAARDPFWLQKITDX 37

Scoring table:
BLOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 200 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-O=/cgm2.1/USPTO.spool/US10042746/runcat.17102005.100127.4856/apd_query.fasta.1.398
-DB=N Geneseq.16Dec04 -QFMT=fastap -SUPFIX=mg -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNIT=bits -START=1 -END=1 -MATRIX=blonum62DX -TRANS=human40.cdi
-LIST=200 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=125
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10042746 @CGN 1.1 586 @runcat.17102005.100127.4856 -NCPU=6 -ICPU=3
-NO MAMP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq.16Dec04:
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001s:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	174	100.0	449	6	ABV98066 Human pan
2	174	100.0	449	6	ABV98700 Human pan
3	174	100.0	517	6	ABV98530 Human pan
4	174	100.0	543	10	ADP16132 Human pan
5	174	100.0	543	10	ADP15896 Human alb

6	174	100.0	543	10	ADP15900	ADP15900 Human alb
7	174	100.0	543	10	ADP16347	ADP16347 Human alb
8	174	100.0	543	10	ADP16130	ADP16130 Human alb
9	174	100.0	543	10	ADP16129	ADP16129 Human alb
10	174	100.0	543	10	ADP16299	ADP16299 Human alb
11	174	100.0	543	10	ADP15899	ADP15899 Human alb
12	174	100.0	543	10	ADP16131	ADP16131 Human alb
13	174	100.0	543	10	ADP16348	ADP16348 Human alb
14	174	100.0	543	10	ADP16133	ADP16133 Human alb
15	174	100.0	543	10	ADP15898	ADP15898 Human alb
16	174	100.0	543	10	ADH21615	ADH21615 Human GLP
17	174	100.0	543	10	ADH21617	ADH21617 Human GLP
18	174	100.0	543	10	ADH21702	ADH21702 Human GLP
19	174	100.0	543	10	ADH21618	ADH21618 Human GLP
20	174	100.0	543	10	ADH21615	ADH21615 Human GLP
21	174	100.0	543	10	ADH21727	ADH21727 Human GLP
22	174	100.0	543	10	ADH21727	ADH21727 Human GLP
23	174	100.0	543	10	ADH21726	ADH21726 Human GLP
24	174	100.0	543	10	ADH22123	ADH22123 Human GLP
25	174	100.0	543	10	ADH21619	ADH21619 Human GLP
26	174	100.0	543	10	ADH22121	ADH22121 Human GLP
27	174	100.0	543	10	ADH22124	ADH22124 Human GLP
28	174	100.0	571	6	ABV98829	ABV98829 Human pan
29	174	100.0	751	6	ABV95109	ABV95109 Human pan
30	174	100.0	825	10	ADP16360	ADP16360 Human alb
31	174	100.0	895	2	AAAT75669	AAAT75669 Rat prepr
32	174	100.0	895	2	AAAT75672	AAAT75672 Human mut
33	174	100.0	955	2	AAAT75673	AAAT75673 Human pre
34	174	100.0	955	2	AAAT75672	AAAT75672 Human pre
35	174	100.0	955	2	AAAT75673	AAAT75673 Human pre
36	174	100.0	955	2	AAAT75675	AAAT75675 Human pre
37	174	100.0	1034	2	AAAT73216	AAAT73216 Rat prepr
38	174	100.0	1034	2	AAAT73216	AAAT73216 Rat prepr
39	174	100.0	1034	2	AAAT73216	AAAT73216 Rat prepr
40	174	100.0	1062	10	ACB56614	ACB56614 Human sly
41	174	100.0	1062	12	ADP15841	ADP15841 Human pol
42	174	100.0	1174	9	ADP11050	ADP11050 Human cdn
43	174	100.0	1525	9	ADP11050	ADP11050 Human cdn
44	174	100.0	2356	3	AAAT5775	AAAT5775 Human gto
45	174	100.0	3798	5	ABV25306	ABV25306 Human pro
46	174	100.0	4146	5	ADP63203	ADP63203 Human ova
47	174	99.4	145	4	AAI19911	AAI19911 Probe #98
48	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
49	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
50	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
51	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
52	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
53	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
54	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
55	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
56	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
57	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
58	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
59	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
60	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
61	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
62	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
63	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
64	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
65	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
66	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
67	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
68	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
69	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
70	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
71	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
72	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
73	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
74	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
75	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
76	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
77	174	99.4	145	4	ABAA4938	ABAA4938 Human foe
78	174	99.4	145	4	ABAA4938	ABAA4938 Human foe

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 17:08:30 ; Search time 2836.5 Seconds

(without alignments)
632.062 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174

Sequence: 1 XXHADGFSDBNNTIIDLNXRPINWLTQKITDX 37

Scoring table:
BLOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapext 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 200 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-Q/cgml1/USPTO.spool/US10042746/runat 17102005 100127 4844/app.query.fasta_1.398
-DB=GenBml -QPMF=fastap -SUFFIX=seq -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62dx -TRANS=human0.cdi -LIST=200
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=125 -MODE=LOCAL
-OUTFM=ptc -NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRS=US10042746 @CCN 1.1 3851 @runat 17102005 100127 4844 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenBml:.*
1: gb_ba:.*
2: gb_hcg:.*
3: gb_in:.*
4: gb_cm:.*
5: gb_cv:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_bcs:.*
12: gb_by:.*
13: gb_un:.*
14: gb_vl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	174	100.0	243 10	RATGIUS
2	174	100.0	543 9	BT006813
3	174	100.0	543 12	BT007507
4	174	100.0	895 6	AR108106

5	174	100.0	955 6	AR108107
6	174	100.0	955 6	AR108109
7	174	100.0	1034 6	A31421
8	174	100.0	1036 6	CO729100
9	174	100.0	1053 10	GP1GG
10	174	100.0	1062 6	AR270649
11	174	100.0	1062 9	HDMGLJC
12	174	100.0	1134 9	BC005278
13	174	100.0	2356 6	AR108119
14	174	100.0	3798 6	CO493428
15	174	100.0	4146 6	CO414344
16	174	100.0	6455 9	HSGJLJC
17	174	100.0	10050 9	HSGJLJC2
18	174	100.0	163681 9	AC007750
19	174	100.0	223513 2	AC111919
20	174	100.0	235433 2	AC097841
21	173	99.4	145 6	CO054796
22	173	99.4	145 6	CO074044
23	173	99.4	145 6	CO104933
24	173	99.4	145 6	CO143637
25	173	99.4	145 6	CO179117
26	173	99.4	145 6	CO203473
27	173	99.4	145 6	CO226837
28	173	99.4	145 6	CO264982
29	173	99.4	145 6	CO302070
30	173	99.4	145 6	CO339262
31	169	97.1	241 10	AY623893
32	169	97.1	668 10	MMPROGLG
33	169	97.1	1102 10	BC012975
34	169	97.1	1116 10	AF276754
35	169	97.1	1118 10	HMGG
36	169	97.1	188169 10	AL928576
37	169	97.1	209762 2	AC115074
38	169	97.1	219014 4	AC024141
39	166	95.4	574 4	AY242124
40	166	95.4	1108 4	BOVGS
41	165	94.8	1104 10	OCOCGLU
42	165	94.8	1133 4	AF308439
43	161	92.5	1056 6	AX147453
44	153	87.9	559 4	AF529185
45	117	67.2	360 6	CO049765
46	117	67.2	360 6	CO064797
47	117	67.2	360 6	CO091744
48	117	67.2	360 6	CO130570
49	117	67.2	360 6	CO169179
50	117	67.2	360 6	CO198311
51	117	67.2	360 6	CO213772
52	117	67.2	360 6	CO252355
53	117	67.2	360 6	CO289502
54	117	67.2	360 6	CO326482
55	115	66.1	1186 5	S78477
56	109	62.6	1360 5	BC075391
57	105	60.3	984 5	AY485816
58	104	59.8	732 5	AY485817
59	104	59.8	892 5	AY485820
60	104	59.8	1050 5	HSU77612
61	103	59.2	1408 5	AF004432
62	99	56.9	974 5	AY485815
63	92	52.9	790 5	AY485819
64	92	52.9	1300 5	AF324209
65	91	52.3	738 5	AF159708
66	90	51.7	796 5	AF159707
67	89	51.1	1014 5	OMU19917
68	89	51.1	1041 5	OMU19917
69	89	51.1	1041 5	S78475
70	88	50.6	520 5	AY485818
71	87	50.6	1045 5	AY485812
72	86	49.4	952 5	AY485809
73	86	49.4	2491 5	AY485821
74	81	46.6	65 6	CO534905
75	80	46.0	383 5	OMU19913
76	80	46.0	383 5	OMU19920
77	80	46.0	400 5	S78473

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 16:34:36 ; Search time: 2275 Seconds
(without alignments)
619.067 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174
Sequence: 1 XXHADGSPSDENMTIIDNIAKDFINMLIQITIDXX 37

Scoring table:
BLOSUM62DX Xgapext 0.5
Xgapop 10.0, Xgapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=x1h
-Q=/cgm2.1/uspro.spool/US10042746/rnat.17102005.100049.4729/app.query.fasta.1.398
-DB=BS1 -QMT=faetap -SUFFIX=ret -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bloums62dx -TRANS=human0.cdi -LIST=500
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=250 -MODE=LOCAL
-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US10042746 @CGN 1.1 4385 @rnat.17102005.100049.4729 -NCPU=6 -ICPU=3
-NO MAP -LAB=BS0DRY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: gb_eat1:*
2: gb_eat2:*
3: gb_hic:*
4: gb_eat3:*
5: gb_eat4:*
6: gb_eat5:*
7: gb_eat6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	174	100.0	224	BU951728
2	174	100.0	310	BU074812
3	174	100.0	340	BU078579
4	174	100.0	378	BU949819
5	174	100.0	384	CB178364
6	174	100.0	389	BO632756
7	174	100.0	391	CA777022
8	174	100.0	400	CB068992
9	174	100.0	401	CA949891

10	174	100.0	403	CA946915
11	174	100.0	409	CB070384
12	174	100.0	419	BM836042
13	174	100.0	420	BQ786903
14	174	100.0	421	CK822370
15	174	100.0	425	CB178016
16	174	100.0	428	BQ271407
17	174	100.0	431	BO632226
18	174	100.0	434	BM352677
19	174	100.0	435	BU074878
20	174	100.0	439	BU077375
21	174	100.0	441	CB842357
22	174	100.0	442	BU786403
23	174	100.0	443	AM190333
24	174	100.0	445	CA865479
25	174	100.0	446	BQ788028
26	174	100.0	450	CA843073
27	174	100.0	450	CA948774
28	174	100.0	451	BM503895
29	174	100.0	452	BQ765791
30	174	100.0	452	CB067109
31	174	100.0	454	AM243578
32	174	100.0	454	BU078231
33	174	100.0	464	CB178614
34	174	100.0	466	CA848770
35	174	100.0	469	CB069665
36	174	100.0	470	BI791800
37	174	100.0	471	BM505325
38	174	100.0	473	CA948241
39	174	100.0	474	BM312561
40	174	100.0	474	BI439035
41	174	100.0	475	BI467273
42	174	100.0	478	BU785166
43	174	100.0	479	BM312257
44	174	100.0	479	CB067193
45	174	100.0	482	CK825195
46	174	100.0	487	CBM312448
47	174	100.0	488	BU786347
48	174	100.0	488	CA841163
49	174	100.0	488	BM509838
50	174	100.0	490	BM504973
51	174	100.0	492	CA772727
52	174	100.0	494	BI791789
53	174	100.0	495	BQ271348
54	174	100.0	496	BI712848
55	174	100.0	497	BI438781
56	174	100.0	498	CB068510
57	174	100.0	499	CA948911
58	174	100.0	499	CA950017
59	174	100.0	501	BI712915
60	174	100.0	501	CA941615
61	174	100.0	504	BM504973
62	174	100.0	506	EG655424
63	174	100.0	507	BU949129
64	174	100.0	508	BG655984
65	174	100.0	508	BU072728
66	174	100.0	508	CA776542
67	174	100.0	509	BI715328
68	174	100.0	509	BM315096
69	174	100.0	509	BM315096
70	174	100.0	511	BQ632620
71	174	100.0	512	CA848560
72	174	100.0	513	BU950509
73	174	100.0	515	CA867509
74	174	100.0	515	CA952216
75	174	100.0	516	CA777150
76	174	100.0	516	CB067101
77	174	100.0	519	BM311172
78	174	100.0	521	BG655407
79	174	100.0	522	CA842549
80	174	100.0	522	CA943101
81	174	100.0	523	BM310964
82	174	100.0	525	CA841460

CA946915	1612f03.x
CB070384	1636e05.y
BM836042	K-EST0111
BQ786903	1151c09.x
CK822370	1686a01.x
CB178016	1624a06.x
BQ271407	1121b06.y
BO632226	1124b11.x
BM352677	1695902.x
BU074878	1m77h03.y
BU077375	1m20e01.y
CB842357	1126a06.y
BU786403	1m54e01.y
AM190333	x161a10.x
CA865479	1140g07.x
BQ788028	1146g09.x
CA843073	1153g03.y
CA948774	1q27f01.y
BM503895	1997b05.y
BQ765791	1134g04.x
CB067109	1q32b10.y
AM243578	x033a10.x
BU078231	1m66a12.y
CB178614	1f37f01.x
CA848770	1f25c05.y
CB069665	1626f05.x
BI791800	1604g03.y
BM505325	1693d01.x
CA948241	1q19g03.y
BM312561	1q17b07.y
BI439035	1c25g02.y
BI467273	1c22c02.x
CA777229	1605h04.y
BM785166	1f41h01.y
BM312257	1q41b09.y
CB067193	1q33d04.y
CK825195	1q46g01.y
CBM312448	1c78f12.x
BU786347	1m53g03.y
CA841163	1p30d08.y
BM509838	1q94f02.y
BM504973	1n73d05.y
BQ955083	1n73d05.y
CA772727	1o84b04.y
BI791789	1e04e11.y
BI771348	1K12f12.y
BI712848	1d98a01.y
BI438781	1c26f01.x
CB068510	1s16c04.y
CA948911	1c29g09.y
CA950017	1165f08.y
BI712915	1d98h02.y
CA941615	1f33f10.y
BM504973	1g98g06.y
BG655424	1b34c02.y
BU949129	1n66c06.x
BG655984	1b35e10.y
BU072728	1m46h11.y
CA776542	1p06e03.y
BI715328	1c31f04.y
BM315096	1q43d08.y
BQ632620	1125f03.y
CA848560	1p36d02.y
BU950509	1o78c02.y
CA867509	1i29c03.y
CA952216	1q16f04.y
CA777150	1p03g09.y
CB067101	1q32a11.y
BM311172	1615g03.y
BG655407	1b39h07.y
CA842549	1q43g10.y
CA943101	1p38e09.y
BM310964	1g59a05.y
CA841460	1q44b03.x

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OM protein - protein search, using sw model

Run on: October 17, 2005, 15:17:48 ; Search time 54.5 Seconds

(without alignments)
282.986 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174
Sequence: 1 XHADGSFDEMTITLNLAKRPFIMWLQTKITDX 37Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1860064 seqs, 416830855 residues

Total number of hits satisfying chosen parameters: 1860064

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database :

Published Applications AA:*

1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep:*

5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	174	100.0	37	14	US-10-042-746-2
2	174	100.0	37	15	US-10-393-524A-11
3	174	100.0	180	16	US-10-793-677-1
4	174	100.0	180	17	US-10-775-180-198
5	174	100.0	180	17	US-10-775-180-199
6	174	100.0	180	17	US-10-775-180-200
7	174	100.0	180	17	US-10-775-180-201
8	174	100.0	180	17	US-10-775-180-202
9	174	100.0	180	17	US-10-775-180-426
10	174	100.0	180	17	US-10-775-180-427
11	174	100.0	180	17	US-10-775-180-428

12	174	100.0	180	17	US-10-775-180-430	Sequence 430, App
13	174	100.0	180	17	US-10-775-180-651	Sequence 651, App
14	174	100.0	180	17	US-10-775-180-675	Sequence 675, App
15	174	100.0	180	17	US-10-775-180-676	Sequence 676, App
16	174	100.0	180	17	US-10-871-709-2	Sequence 2, Appl
17	174	100.0	180	18	US-10-775-204-630	Sequence 630, App
18	174	100.0	180	18	US-10-775-204-632	Sequence 632, App
19	174	100.0	180	18	US-10-775-204-633	Sequence 633, App
20	174	100.0	180	18	US-10-775-204-634	Sequence 634, App
21	174	100.0	180	18	US-10-775-204-1246	Sequence 1246, App
22	174	100.0	180	18	US-10-775-204-1247	Sequence 1247, App
23	174	100.0	180	18	US-10-775-204-1248	Sequence 1248, App
24	174	100.0	180	18	US-10-775-204-1249	Sequence 1249, App
25	174	100.0	180	18	US-10-775-204-1250	Sequence 1250, App
26	174	100.0	180	18	US-10-775-204-1251	Sequence 1251, App
27	174	100.0	180	18	US-10-775-204-1277	Sequence 1277, App
28	174	100.0	180	18	US-10-775-204-1775	Sequence 1775, App
29	174	100.0	180	20	US-11-060-291-4	Sequence 1776, App
30	172	98.9	47	9	US-09-864-761-33848	Sequence 4, Appl
31	171	98.3	34	16	US-10-203-808-5	Sequence 33848, A
32	171	98.3	34	16	US-10-203-808-15	Sequence 5, Appl
33	171	98.3	34	16	US-10-737-290-175	Sequence 15, Appl
34	171	98.3	34	20	US-11-066-697-346	Sequence 175, App
35	171	98.3	34	20	US-10-424-599-172728	Sequence 346, App
36	170	97.7	33	14	US-10-295-820-1	Sequence 172728, A
37	170	97.7	33	14	US-10-042-746-4	Sequence 1, Appl
38	170	97.7	33	14	US-10-042-746-3	Sequence 3, Appl
39	170	97.7	33	14	US-10-293-941-2	Sequence 4, Appl
40	170	97.7	33	15	US-10-201-288-30	Sequence 2, Appl
41	170	97.7	33	15	US-10-393-524A-3	Sequence 30, Appl
42	170	97.7	33	15	US-10-393-524A-12	Sequence 3, Appl
43	170	97.7	33	15	US-10-393-524A-13	Sequence 12, Appl
44	170	97.7	33	16	US-10-685-368-1	Sequence 13, Appl
45	170	97.7	33	16	US-10-730-215-6	Sequence 1, Appl
46	170	97.7	33	16	US-10-203-808-1	Sequence 6, Appl
47	170	97.7	33	16	US-10-203-808-3	Sequence 1, Appl
48	170	97.7	33	16	US-10-203-808-4	Sequence 3, Appl
49	170	97.7	33	16	US-10-203-808-14	Sequence 4, Appl
50	170	97.7	33	17	US-10-847-120-3	Sequence 14, Appl
51	170	97.7	33	17	US-10-919-325-31	Sequence 31, Appl
52	170	97.7	33	20	US-11-066-697-345	Sequence 31, Appl
53	170	97.7	45	18	US-10-993-127-2	Sequence 345, App
54	170	97.7	240	18	US-10-993-127-2	Sequence 4, Appl
55	167	96.0	34	16	US-10-203-808-10	Sequence 2, Appl
56	167	96.0	34	16	US-10-203-808-12	Sequence 10, Appl
57	167	96.0	34	16	US-10-203-808-13	Sequence 12, Appl
58	166	95.4	33	15	US-10-393-524A-14	Sequence 23, Appl
59	166	95.4	33	15	US-10-203-808-7	Sequence 14, Appl
60	166	95.4	33	16	US-10-203-808-8	Sequence 7, Appl
61	166	95.4	33	16	US-10-203-808-13	Sequence 8, Appl
62	164	94.3	33	16	US-10-203-808-6	Sequence 13, Appl
63	164	94.3	33	16	US-10-203-808-16	Sequence 16, Appl
64	164	94.3	33	16	US-10-203-808-17	Sequence 17, Appl
65	164	94.3	33	16	US-10-203-808-18	Sequence 18, Appl
66	164	94.3	33	16	US-10-203-808-20	Sequence 20, Appl
67	164	94.3	33	16	US-10-203-808-21	Sequence 21, Appl
68	164	94.3	33	16	US-10-203-808-24	Sequence 24, Appl
69	164	94.3	33	16	US-10-203-808-26	Sequence 26, Appl
70	164	94.3	33	16	US-10-203-808-27	Sequence 27, Appl
71	164	94.3	34	16	US-10-997-078-35	Sequence 35, Appl
72	163	93.7	33	16	US-10-203-808-19	Sequence 37, Appl
73	163	93.7	33	16	US-10-203-808-22	Sequence 37, Appl
74	163	93.7	33	18	US-10-997-078-16	Sequence 38, Appl
75	163	93.7	33	16	US-10-730-215-7	Sequence 38, Appl
76	162	93.1	33	16	US-10-203-808-9	Sequence 7, Appl
77	160	92.0	33	16	US-10-203-808-11	Sequence 9, Appl
78	160	92.0	33	16	US-10-203-808-18	Sequence 11, Appl
79	160	92.0	33	16	US-10-203-808-25	Sequence 25, Appl
80	160	92.0	34	18	US-10-997-078-38	Sequence 25, Appl
81	159	91.4	32	17	US-10-768-974-17	Sequence 37, Appl
82	159	91.4	33	18	US-10-997-078-17	Sequence 37, Appl
83	158	90.8	31	17	US-10-768-974-38	Sequence 38, Appl
84	154	88.5	33	17	US-10-847-220-12	Sequence 429, App

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OM protein - protein search, using sw model

Run on: October 16, 2005, 14:54:46 ; Search time 52.5 Seconds

(without alignments)
52.610 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174

Sequence: 1 XXHADGSFSDENMTILDNLAXRDPINWLIQTITDX 37

Scoring table: BLOSUM62DX

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database :

Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	174	100.0	180	3	US-08-784-582-58
7	174	100.0	180	3	US-08-784-582-61
8	174	100.0	360	3	US-08-784-582-73
9	172	98.9	48	2	US-08-808-825-8
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12	170	97.7	33	2	US-08-669-790C-4
13	170	97.7	33	2	US-08-808-825-5
14	170	97.7	33	2	US-08-808-825-6
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21	170	97.7	33	4	US-09-693-238-1
22	166	95.4	33	1	US-08-669-791C-5
23	162	92.1	33	2	US-08-808-825-7
24	115	66.1	37	2	US-08-422-540A-1
25	115	66.1	37	2	US-08-422-540A-4
26	115	66.1	37	2	US-08-422-540A-5
27	100	57.5	37	2	US-08-669-790C-1

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41	78	44.8	33	3	US-09-258-750-12	Sequence 12, Appl
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72	77	44.3	38	3	US-09-258-750-82	Sequence 82, Appl
73	77	44.3	38	4	US-09-398-111-43	Sequence 43, Appl
74	77	44.3	38	4	US-09-398-111-52	Sequence 52, Appl
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76	77	44.3	38	4	US-09-398-111-70	Sequence 70, Appl
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79	77	44.3	39	3	US-09-258-750-44	Sequence 44, Appl
80	77	44.3	39	3	US-09-258-750-53	Sequence 53, Appl
81	77	44.3	39	3	US-09-258-750-62	Sequence 62, Appl
82	77	44.3	39	3	US-09-258-750-71	Sequence 71, Appl
83	77	44.3	39	3	US-09-258-750-89	Sequence 89, Appl
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85	77	44.3	39	4	US-09-398-111-35	Sequence 35, Appl
86	77	44.3	39	4	US-09-398-111-44	Sequence 44, Appl
87	77	44.3	39	4	US-09-398-111-53	Sequence 53, Appl
88	77	44.3	39	4	US-09-398-111-62	Sequence 62, Appl
89	77	44.3	39	4	US-09-398-111-71	Sequence 71, Appl
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94	77	44.3	40	3	US-09-258-750-63	Sequence 63, Appl
95	77	44.3	40	3	US-09-258-750-72	Sequence 72, Appl
96	77	44.3	40	4	US-09-398-111-36	Sequence 36, Appl
97	77	44.3	40	4	US-09-398-111-45	Sequence 45, Appl
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100	77	44.3	40	4	US-09-398-111-72	Sequence 72, Appl

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OM protein - protein search, using sw model

Run on: October 17, 2005, 12:43:07 ; Search time 56 Seconds
(without alignments) 255.538 Million cell updates/sec

Title: US-10-042-746-2

Sequence: 1 XXHADGSEFSDENMTILDNLAXRPRINMLIQTKITDXX 37

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	174	100.0	180	AAW22079	AAW22079 Rat prepr
5	174	100.0	180	AAW22080	AAW22080 Human pre
6	174	100.0	180	AAV39812	AAV39812 Preproglu
7	174	100.0	180	AAW26773	AAW26773 Rat prepr
8	174	100.0	180	AAW26774	AAW26774 Human pre
9	174	100.0	180	AAW26775	AAW26775 Mutant hu
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22	174	100.0	180	ADP15331	ADP15331 Human alb
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26	174	100.0	180	ADH21630	Adh21630 Human GLP
27	174	100.0	180	ADH21401	Adh21401 Human GLP
28	174	100.0	180	ADH21404	Adh21404 Human GLP
29	174	100.0	180	ADH21402	Adh21402 Human GLP
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31	174	100.0	180	ADH21854	Adh21854 Human GLP
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76	174	100.0	180	ADH21879	Adh21879 Human GLP
77	174	100.0	180	ADH21879	Adh21879 Human GLP
78	174	100.0	180	ADH21879	Adh21879 Human GLP
79	174	100.0	180	ADH21879	Adh21879 Human GLP
80	174	100.0	180	ADH21879	Adh21879 Human GLP
81	174	100.0	180	ADH21879	Adh21879 Human GLP
82	174	100.0	180	ADH21879	Adh21879 Human GLP
83	174	100.0	180	ADH21879	Adh21879 Human GLP
84	174	100.0	180	ADH21879	Adh21879 Human GLP
85	174	100.0	180	ADH21879	Adh21879 Human GLP
86	174	100.0	180	ADH21879	Adh21879 Human GLP
87	174	100.0	180	ADH21879	Adh21879 Human GLP
88	174	100.0	180	ADH21879	Adh21879 Human GLP
89	174	100.0	180	ADH21879	Adh21879 Human GLP
90	174	100.0	180	ADH21879	Adh21879 Human GLP
91	174	100.0	180	ADH21879	Adh21879 Human GLP
92	174	100.0	180	ADH21879	Adh21879 Human GLP
93	174	100.0	180	ADH21879	Adh21879 Human GLP
94	174	100.0	180	ADH21879	Adh21879 Human GLP
95	174	100.0	180	ADH21879	Adh21879 Human GLP
96	174	100.0	180	ADH21879	Adh21879 Human GLP
97	174	100.0	180	ADH21879	Adh21879 Human GLP
98	174	100.0	180	ADH21879	Adh21879 Human GLP

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OM protein - protein search, using sw model

Run on: October 16, 2005, 10:55:31 ; Search time 38.5 Seconds

(without alignments)
92.468 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174
Sequence: 1 XXHADGSPDEMTILDNLAXRPFIMWLTQKTDKX 37

Scoring table: BIOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 200 summaries

Database :

1: PIR 79: *
2: D1r1: *
3: D1r2: *
4: D1r3: *
5: D1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	174	100.0	180	1	GCGR
2	174	100.0	180	1	GCHU
3	174	100.0	180	1	GCHT
4	169	97.1	180	1	GCHY
5	169	97.1	180	2	AS7294
6	165	94.8	180	1	GCRIDU
7	164	94.3	158	1	GCPI
8	159	91.4	180	1	GCHU
9	115	66.1	206	2	IS1301
10	90	51.7	101	1	GCFGB
11	89	51.1	178	2	IS1057
12	89	51.1	178	2	IS1058
13	86	49.4	36	1	GCFI
14	80	46.0	66	2	IS1093
15	78	44.8	60	1	GCONC
16	77	44.3	29	2	S07211
17	76	43.7	30	2	S44473
18	76	43.7	63	1	GCHD
19	76	43.7	69	1	GCHD69
20	76	43.7	122	1	GCAF2
21	76	43.7	151	1	GCHH
22	75	43.1	29	1	GCHP
23	75	43.1	29	1	GCHN
24	74	42.5	72	1	GCHX
25	73	42.0	144	1	JN0589
26	72	41.4	153	1	A28406
27	71	40.8	42	1	GIBO
28	71	40.8	42	1	GIBG
29	70	40.2	144	2	S71426

30	69	39.7	29	1	GCOPV	glucagon - North A
31	69	39.7	29	2	A91740	glucagon - turkey
32	69	39.7	29	2	C39258	glucagon - common
33	69	39.7	29	2	A91742	glucagon - Arabian
34	69	39.7	29	2	A91741	glucagon - rabbit
35	69	39.7	124	1	GCAF	glucagon 1 precurs
36	68	39.1	29	1	A61583	glucagon - ostrich
37	68	39.1	29	1	GCDC	glucagon - duck
38	68	39.1	29	1	GCHS	glucagon - slider
39	67	38.5	29	2	S39018	glucagon - bowfin
40	66	37.9	30	2	G61125	glucagon-like pept
41	66	37.9	30	2	B61125	glucagon-like pept
42	66	37.9	87	1	GCHS	glucagon precursor
43	64	36.8	29	1	GCHS	glucagon - Europea
44	64	36.8	29	2	A61135	glucagon - bigeye
45	62	35.6	39	1	GCHS	glucagon - Chinchi
46	62	35.6	39	1	HMCH32	exendin-3 - Mexica
47	62	35.6	2172	2	T20145	hypothetical prote
48	61	35.1	29	2	C60840	glucagon I - Europ
49	61	35.1	502	2	H75290	hypothetical prote
50	59	33.9	850	2	T51541	hypothetical prote
51	58	33.3	170	1	VRRT	vasoactive intesti
52	58	33.3	170	2	A60037	vasoactive intesti
53	57	32.8	39	1	HMCH4G	exendin-4 - Gila m
54	57	32.8	55	1	VRGP	vasoactive intesti
55	57	32.8	145	2	A60038	vasoactive intesti
56	57	32.8	170	1	VRHU	vasoactive intesti
57	57	32.8	679	2	C71413	hypothetical prote
58	57	32.8	1260	2	T01334	hypothetical prote
59	56	32.2	31	2	S44472	glucagon G2 - Nort
60	55	31.6	55	1	VRBB	vasoactive intesti
61	55	31.6	58	1	VRPG	vasoactive intesti
62	55	31.6	765	2	G64228	hypothetical prote
63	54.5	31.0	1088	2	C83054	glucagon G1 - Nort
64	54	31.0	31	2	S44471	vasoactive intesti
65	54	31.0	55	1	VRBO	vasoactive intesti
66	54	31.0	55	1	VRSH	heat-stable entero
67	54	31.0	1075	1	ORITHX	glycoprotein H pre
68	53.5	30.7	419	2	S74329	hypothetical prote
69	53.5	30.7	808	1	J02043	hypothetical prote
70	53	30.5	342	2	T16444	hypothetical prote
71	53	30.5	464	2	D82375	thiophene and fura
72	53	30.5	494	2	B82874	conserved hypothet
73	52.5	30.2	79	2	AB1982	hypothetical prote
74	52.5	30.2	460	2	T39462	argininosuccinate
75	52.5	30.2	1151	2	T24541	hypothetical prote
76	52	29.9	36	2	D60840	glucagon II - Euro
77	52	29.9	298	2	P69502	hypothetical prote
78	52	29.9	344	2	S64931	hypothetical prote
79	52	29.9	388	2	H64427	hypothetical prote
80	52	29.9	512	2	AC3203	IS3 family transpo
81	52	29.9	512	2	AD2835	IS3 family transpo
82	52	29.9	512	2	AD3049	IS3 family transpo
83	52	29.9	512	2	G97612	probable transposa
84	52	29.9	512	2	G98236	probable transposa
85	52	29.9	518	2	D97310	ATPase component o
86	52	29.9	648	2	T09036	hypothetical prote
87	52	29.9	1077	2	S66842	hypothetical prote
88	51.5	29.6	1999	2	AB2018	neuropeptides prec
89	51	29.3	173	2	S34767	conserved hypothet
90	51	29.3	323	2	B83288	hypothetical prote
91	51	29.3	325	2	B90764	conserved hypothet
92	51	29.3	336	2	B70102	unknown protein en
93	51	29.3	349	2	D85678	hypothetical prote
94	51	29.3	349	2	H85626	hypothetical prote
95	51	29.3	349	2	B90819	hypothetical prote
96	51	29.3	349	2	E90912	hypothetical prote
97	51	29.3	662	2	T33900	hypothetical prote
98	51	29.3	990	2	T05197	hypothetical prote
99	51	29.3	1007	2	G96606	disease resistance
100	50.5	29.0	165	2	AG0619	probable bacteriop
101	50.5	29.0	1369	2	T32338	hypothetical prote
102	50.5	29.0	1600	2	AB3281	glutamate dehydrog

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OM protein - protein search, using SW model

Run on: October 16, 2005, 10:03:46 ; Search time 199.5 Seconds

(without alignments)
94.972 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174
Sequence: 1 XXHADGSPFEDENITLNLAXRPFINMLIQTITDX 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	174	100.0	180	1	GLUC_CAVPO
2	174	100.0	180	1	GLUC_HUMAN
3	174	100.0	180	1	GLUC_RAT
4	169	97.1	80	2	Q6IUP8
5	169	97.1	180	1	GLUC_MESAU
6	169	97.1	180	1	GLUC_MOUSE
7	166	95.4	180	1	GLUC_BOVIN
8	166	95.4	180	1	GLUC_PIG
9	165	94.8	180	1	GLUC_CANPA
10	165	94.8	180	1	GLUC_OCTDR
11	153	87.9	176	1	GLUC_SHEEP
12	115	66.1	206	1	GLUC_CHICK
13	109	62.6	266	2	Q6DIZ4
14	105	60.3	145	2	Q6RYB5
15	104	59.8	124	2	Q6RYB1
16	104	59.8	170	2	Q6RYB4
17	104	59.8	204	1	GLUC_HELISU
18	103	59.2	266	1	GLUI_XENILA
19	99	56.9	153	2	Q6RYB6
20	92	52.9	149	2	Q6RYB2
21	92	52.9	220	2	Q6RYB3
22	91	52.3	120	2	GLU2_PETMA
23	90	51.7	103	1	GLUI_PETMA
24	90	51.7	160	1	GLUI_PETMA
25	89	51.1	178	1	GLUI_ONCMY
26	89	51.1	178	1	GLU2_ONCMY
27	88	50.6	173	2	Q6RYB3
28	87	50.0	173	2	Q6RYB9
29	86	49.4	36	1	GLUC_HYDCO
30	86	49.4	176	2	Q6RYB0
31	86	49.4	176	2	Q6RYC2

32	80	46.0	62	1	GLUC_SEYCA
33	80	46.0	66	2	Q788W6
34	80	46.0	72	2	Q91409
35	79	45.4	122	2	Q6RYB8
36	78	44.8	68	1	GLUC_ONCKI
37	78	44.8	219	1	GLU2_XENILA
38	77	44.3	29	1	GLUC_TORMA
39	76	43.7	30	2	Q7LZN3
40	76	43.7	122	1	GLU2_IOPAM
41	75	43.1	29	1	GLUC_CALMI
42	75	43.1	71	1	GLUC_ICTPU
43	75	43.1	71	1	GLUC_PIANE
44	74	42.5	45	2	Q6PPF4
45	74	42.5	78	1	GLUC_LEPSP
46	74	42.5	120	2	Q6RYB7
47	73	42.0	121	1	GLUC_CARAU
48	73	42.0	144	1	GIP_RAT
49	72	41.4	121	2	Q6RYC1
50	72	41.4	121	2	Q9DD86
51	72	41.4	153	1	GIP_HUMAN
52	72	41.4	153	2	Q6NTD3
53	71	40.8	36	1	GLUI_ORENT
54	71	40.8	42	1	GIP_BOVIN
55	71	40.8	42	1	GIP_PIG
56	70	40.2	29	1	GLUC_LAMFL
57	70	40.2	130	2	Q9CVF1
58	70	40.2	144	1	GIP_MOUSE
59	70	40.2	144	2	Q9DB87
60	70	40.2	500	2	Q649W5
61	69	39.7	29	1	GLUC_CAMPB
62	69	39.7	29	1	GLUC_DIDMA
63	69	39.7	29	1	GLUC_MELGA
64	69	39.7	29	1	GLUC_RABIT
65	69	39.7	29	1	GLUC_SALSC
66	69	39.7	123	2	Q6RYA9
67	69	39.7	124	1	GLUI_LOPM
68	68	39.1	29	1	GLUC_ANAPL
69	67	38.5	96	2	Q9DG43
70	67	38.5	96	2	Q9DG43
71	66	37.9	30	1	GLUM_ANGAN
72	66	37.9	96	1	GLUC_MYOSC
73	66	37.9	96	1	GLUC_PLARE
74	64	36.8	29	1	GLUC_PLARE
75	64	36.8	87	2	Q7SZU6
76	62	35.6	29	1	GLUC_CHIRB
77	62	35.6	39	1	EXB3_HELMO
78	62	35.6	2162	2	Q6N5I5
79	61	35.3	145	2	Q7NIM1
80	61	35.1	502	2	Q9RS41
81	60	34.5	170	1	VIP_BOVIN
82	60	34.5	626	2	Q9OWG7
83	59.5	34.2	2980	2	Q8IAK3
84	59	33.9	87	1	EXB4_HELISU
85	59	33.9	200	1	VIP_CHICK
86	59	33.9	387	2	Q8FSR2
87	59	33.9	850	2	Q9LPL5
88	58	33.3	153	2	Q7TSR4
89	58	33.3	170	1	VIP_MOUSE
90	58	33.3	170	1	VIP_RAT
91	58	33.3	171	2	Q9DZT7
92	58	33.3	175	1	PACA_CHICK
93	58	33.3	200	1	VIP_MELGA
94	57	32.8	145	2	Q7M2Y9
95	57	32.8	170	1	VIP_HUMAN
96	57	32.8	679	2	Q7ZV88
97	57	32.8	202	2	Q23352
98	57	32.8	787	2	Q94C98
99	57	32.8	1260	2	Q81307
100	56.5	32.5	559	2	Q8ZMP5
101	56.5	32.5	608	2	Q6CTU0
102	56	32.2	31	2	Q7LZN2
103	56	32.2	1128	2	Q7T5I2
104	56	32.2	77	2	VIP_HUMAN

P09687 bcylicorhinu
Q788W6 oncorhynchus
Q91409 oncorhynchus
Q6RYB8 ictalurinus p
P07449 oncorhynchus
Q42144 xenopus lae
P09567 toipeda mar
Q712N3 polyodon sp
P04092 lophius ame
P13189 callorhynch
P04093 ictalurinus p
P81880 piactatus m
Q6PPF4 capra hircu
P09566 lepisosteus
Q6RYB7 ictalurinus p
P79695 carassius a
Q06145 rattus norv
Q6RYC1 sebaestes ca
Q9dd6 brachydanio
P09681 homo sapien
Q6ntd3 homo sapien
P81026 oreochromis
P09680 bos taurus
P01281 sus scrofa
Q9PRQ9 lampetra fl
Q9CVF1 mus musculu
P48756 mus musculu
Q9DB87 mus musculu
Q849W5 escherichia
P68273 camelus dro
P18108 didelphis m
P68260 meleagris g
P68274 oryctolagus
P68275 salmistr sci
Q6RYA9 sebaestes ca
P01278 lophius ame
P01278 anas platyr
P33528 amia calva
Q9DG43 ambloplites
P63294 anguilla an
P63295 anguilla ro
P09686 myoxocephal
P23062 platichthys
Q7SZU6 heloderma h
P13297 chinchilla
P20394 heloderma h
Q09515 caenothabdi
Q7NIM1 photorhabdi
Q97841 deinococcus
P81401 bos taurus
Q9OWG7 cynops pyrr
Q8IAK3 plasmodium
P23349 heloderma s
P48143 gallus galli
Q0F82 corynebacte
Q9LFL5 arabidopsis
Q7LFR4 arvicantis
P12648 mus musculu
P01289 rattus norv
Q9DZT7 mus musculu
P41554 glaucagon-
P45644 meleagris g
Q7M2Y9 macaca fasc
P01282 homo sapien
Q7ZV88 xenopus lae
Q23352 arabidopsis
Q94C98 arabidopsis
Q81307 arabidopsis
Q8ZMP5 salmoneilla
Q6CTU0 kluyveromyc
Q7LZN2 polyodon sp
Q7T5I2 cryophleb

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OM protein - protein search, using sw model

Run on: October 16, 2005, 10:55:31 ; Search time 38.5 Seconds

(without alignments)
92.468 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174
Sequence: 1 XXHADGSPDENNTIIDNLAAXRPFIMLTQITDXX 37

Scoring table: BLOSUM62DX
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database :
1: PIR 79: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	174	100.0	180	1 GCGP	glucagon precursor
2	174	100.0	180	1 GCHU	glucagon precursor
3	174	100.0	180	1 GCHU	glucagon precursor
4	169	97.1	180	1 GCHV	glucagon precursor
5	169	97.1	180	2 A57294	glucagon precursor
6	165	94.8	180	1 GCRITU	glucagon precursor
7	164	94.3	158	1 GCPG	glucagon precursor
8	159	91.4	180	1 GCHO	glucagon precursor
9	115	66.1	206	2 I51301	proglucagon - chic
10	90	51.7	101	1 GCRB	glucagon precursor
11	89	51.1	178	2 I51057	glucagon II precu
12	86	49.4	178	2 I51058	glucagon I precu
13	86	49.4	36	1 GCFI	glucagon-36 - spot
14	80	46.0	66	2 I51093	glucagon - chinook
15	78	44.8	60	1 GCONC	glucagon precursor
16	77	44.3	29	2 S07211	glucagon - marbled
17	76	43.7	30	2 S44473	glucagon-like pept
18	76	43.7	63	1 GCDIC	glucagon precursor
19	76	43.7	69	1 GCDG69	glucagon-69 - dog
20	76	43.7	122	1 GCAF2	glucagon 2 precu
21	76	43.7	151	1 GCDH	glucagon precursor
22	75	43.1	29	1 GCDP	glucagon - smaller
23	75	43.1	29	1 GCEN	glucagon - elephant
24	74	42.5	72	1 GCGXA	glucagon precursor
25	73	42.0	144	1 JN0589	glucose-dependent
26	72	41.4	153	1 A28406	gastric inhibitory
27	71	40.8	42	1 GIBO	gastric inhibitory
28	71	40.8	42	1 GIPG	gastric inhibitory
29	70	40.2	144	2 S71426	glucose-dependent

30	69	39.7	29	1 GCOV	glucagon - North A
31	69	39.7	29	2 A91740	glucagon - turkey
32	69	39.7	29	2 C39258	glucagon - common
33	69	39.7	29	2 A91742	glucagon - Arabian
34	69	39.7	29	2 A91741	glucagon - rabbit
35	69	39.7	124	1 GCAF	glucagon 1 precu
36	68	39.1	29	1 A61583	glucagon - ostrich
37	68	39.1	29	1 GCDK	glucagon - duck
38	68	39.1	29	1 GCDT	glucagon - slider
39	67	38.5	29	2 S39018	glucagon - bowfin
40	67	37.9	30	2 C61125	glucagon-like pept
41	66	37.9	30	2 B61125	glucagon-like pept
42	66	37.9	87	1 GCFIS	glucagon precursor
43	64	36.8	29	1 GCFIS	glucagon - Europea
44	64	36.8	29	2 A61135	glucagon - bigeye
45	62	35.6	29	1 GCB	glucagon - Chinchi
46	62	35.6	39	1 HMG32	extending-3 - Mexica
47	62	35.6	2172	2 T20145	glucagon I - Europ
48	61	35.1	29	2 C60840	hypothetical prote
49	61	35.1	502	2 H75290	hypothetical prote
50	59	33.9	850	2 T51541	hypothetical prote
51	58	33.3	170	1 VRRT	vasoactive intesti
52	58	33.3	170	2 A60037	vasoactive intesti
53	57	32.8	39	1 HMG4G	extending-4 - Gila m
54	57	32.8	55	1 VRGP	vasoactive intesti
55	57	32.8	145	2 A60038	vasoactive intesti
56	57	32.8	170	1 VRHU	vasoactive intesti
57	57	32.8	679	2 C71413	hypothetical prote
58	57	32.8	1260	2 T01334	hypothetical prote
59	56	32.2	31	2 S44472	glucagon G2 - Nort
60	55	31.6	55	1 VRB	vasoactive intesti
61	55	31.6	55	1 VRP	vasoactive intesti
62	55	31.6	765	2 G64228	hypothetical prote
63	54.5	31.0	1088	2 C83054	glucagon G1 - Nort
64	54	31.0	31	2 S44471	vasoactive intesti
65	54	31.0	55	1 VRBO	vasoactive intesti
66	54	31.0	55	1 VRSH	vasoactive intesti
67	54	31.0	1075	1 OYRTX	heat-stable entero
68	53.5	30.7	419	2 S74329	hypothetical prote
69	53.5	30.7	808	1 JQ02043	glycoprotein H pre
70	53	30.5	342	2 T16444	hypothetical prote
71	53	30.5	464	2 D82375	thiophene and fura
72	53	30.5	494	2 B82874	conserved hypothec
73	52.5	30.2	79	2 AB1982	hypothetical prote
74	52.5	30.2	460	2 T39462	argininosuccinate
75	52.5	30.2	1151	2 T24541	hypothetical prote
76	52	29.9	36	2 D60840	glucagon II - Euro
77	52	29.9	298	2 F69502	hypothetical prote
78	52	29.9	344	2 S64931	hypothetical prote
79	52	29.9	388	2 H64427	hypothetical prote
80	52	29.9	512	2 AC3203	IS3 family transpo
81	52	29.9	512	2 AD2835	IS3 family transpo
82	52	29.9	512	2 AD3049	IS3 family transpo
83	52	29.9	512	2 G97612	probable transpos
84	52	29.9	512	2 G98236	probable transpos
85	52	29.9	518	2 D97310	ATPase component o
86	52	29.9	648	2 T09036	hypothetical prote
87	52	29.9	1077	2 S66442	hypothetical prote
88	51.5	29.6	1999	2 AB2018	hypothetical prote
89	51	29.3	173	2 S34767	neuropeptides prec
90	51	29.3	333	2 B83288	conserved hypothec
91	51	29.3	325	2 B90764	hypothetical prote
92	51	29.3	336	2 B70102	conserved hypothec
93	51	29.3	349	2 D85678	unknown protein en
94	51	29.3	349	2 H85626	hypothetical prote
95	51	29.3	349	2 B90819	hypothetical prote
96	51	29.3	349	2 B90912	hypothetical prote
97	51	29.3	662	2 T33900	hypothetical prote
98	51	29.3	990	2 T05197	hypothetical prote
99	51	29.3	1007	2 G96606	disease resistance
100	50.5	29.0	165	2 AG0619	probable bacteriop
101	50.5	29.0	1369	2 T32338	hypothetical prote
102	50.5	29.0	1600	2 AB3281	glutamate dehydrog

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CM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 17:17:30 ; Search time 490 Seconds

(without alignments)
529.404 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155

Sequence:

1 XXHADGFSFSDENMTXLDLAXXDFINWLXXTKRTDX 37

Scoring table:

BLOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 8766186 seqs, 3505510206 residues

Total number of hits satisfying chosen parameters: 17532372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 200 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO.spool/US10042746/runat_17102005_100128_4884/app_query.fasta_1.398
-DB=Published Applications NA -OPMT=fastcap -SUFFIX=rmph -MINMATCH=0.1
-LOOCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloms62DX
-TRANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 ALIGN=125 -MODB=LOCAL -OUTFMT=ptc -NORM=ext -HABSIZE=500
-MINLEN=0 -MAXLEN=200000000
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-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA.*
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/FCOT_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US10A_NEW_PUB.seq.*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155	100.0	449	14	US-10-060-036-3474 Sequence 3477, Ap
2	155	100.0	449	14	US-10-060-036-4108 Sequence 4109, Ap
3	155	100.0	517	14	US-10-060-036-3938 Sequence 3938, Ap
4	155	100.0	543	21	US-10-775-180-60 Sequence 60, Appl
5	155	100.0	543	21	US-10-775-180-61 Sequence 61, Appl
6	155	100.0	543	21	US-10-775-180-62 Sequence 62, Appl
7	155	100.0	543	21	US-10-775-180-63 Sequence 63, Appl
8	155	100.0	543	21	US-10-775-180-412 Sequence 412, Ap
9	155	100.0	543	21	US-10-775-180-413 Sequence 413, Ap
10	155	100.0	543	21	US-10-775-180-414 Sequence 414, Ap
11	155	100.0	543	21	US-10-775-180-415 Sequence 415, Ap
12	155	100.0	543	21	US-10-775-180-416 Sequence 416, Ap
13	155	100.0	543	21	US-10-775-180-499 Sequence 499, Ap
14	155	100.0	543	21	US-10-775-180-523 Sequence 523, Ap
15	155	100.0	543	21	US-10-775-180-524 Sequence 524, Ap
16	155	100.0	543	21	US-10-775-204-198 Sequence 198, Ap
17	155	100.0	543	22	US-10-775-204-200 Sequence 200, Ap
18	155	100.0	543	22	US-10-775-204-201 Sequence 201, Ap
19	155	100.0	543	22	US-10-775-204-202 Sequence 202, Ap
20	155	100.0	543	22	US-10-775-204-1216 Sequence 1216, Ap
21	155	100.0	543	22	US-10-775-204-1217 Sequence 1217, Ap
22	155	100.0	543	22	US-10-775-204-1218 Sequence 1218, Ap
23	155	100.0	543	22	US-10-775-204-1219 Sequence 1219, Ap
24	155	100.0	543	22	US-10-775-204-1230 Sequence 1220, Ap
25	155	100.0	543	22	US-10-775-204-1391 Sequence 1391, Ap
26	155	100.0	543	22	US-10-775-204-1439 Sequence 1439, Ap
27	155	100.0	543	22	US-10-775-204-1440 Sequence 1440, Ap
28	155	100.0	673	14	US-10-060-036-4237 Ap Sequence 4237, Ap
29	155	100.0	751	14	US-10-060-036-517 Sequence 517, Ap
30	155	100.0	825	22	US-10-775-204-1452 Sequence 1452, Ap
31	155	100.0	1034	21	US-10-871-709-1 Sequence 1, Appl
32	155	100.0	1062	17	US-10-305-720-1212 Sequence 1212, Ap
33	155	100.0	1174	9	US-09-981-353-169 Sequence 169, Ap
34	155	100.0	1525	9	US-09-981-353-168 Sequence 168, Ap
35	155	100.0	3798	20	US-10-357-930-25295 Sequence 25295, A
36	155	100.0	4146	10	US-09-814-353-21415 Sequence 21415, A
37	155	100.0	10370	22	US-10-737-082-7 Sequence 7, Appl
38	155	100.0	10370	22	US-10-765-790-7 Sequence 7, Appl
39	154	99.4	145	9	US-09-864-761-17367 Sequence 17367, A
40	152	98.1	102	22	US-10-997-078-55 Sequence 55, Appl
41	152	98.1	472	18	US-10-424-599-29886 Sequence 29886, A
42	151	97.4	99	22	US-10-997-078-56 Sequence 56, Appl
43	151	97.4	160	22	US-10-993-127-3 Sequence 3, Appl
44	151	97.4	6004	22	US-10-993-127-1 Sequence 1, Appl
45	148	95.5	102	22	US-10-997-078-58 Sequence 58, Appl
46	147	94.8	99	22	US-10-997-078-57 Sequence 57, Appl
47	147	94.8	360	9	US-09-864-761-575 Sequence 575, Ap
48	105	67.7	626	11	US-09-869-034-2554 Sequence 2554, Ap
49	86	55.5	180	17	US-10-378-094-50 Sequence 50, Appl
50	84	54.2	180	17	US-10-378-094-51 Sequence 51, Appl
51	84	54.2	180	16	US-10-029-386-23164 Sequence 23164, A
52	79	51.0	436	9	US-09-925-297-49 Sequence 29, Appl
53	79	51.0	576	16	US-10-029-386-9464 Sequence 9464, Ap
54	79	51.0	1021	17	US-10-321-039-41 Sequence 41, Appl
55	76	50.3	665	10	US-09-908-975-4540 Sequence 4540, Ap
56	76	49.0	294	9	US-09-777-564-883 Sequence 883, Ap
57	76	49.0	294	14	US-10-015-219-883 Sequence 883, Ap
58	76	49.0	358	17	US-10-307-719A-17 Sequence 17, Appl
59	76	49.0	424	17	US-10-307-719A-15 Sequence 15, Appl
60	76	49.0	576	17	US-10-307-719A-13 Sequence 13, Appl
61	74	47.7	112	14	US-10-093-958-18 Sequence 18, Appl
62	74	47.7	180	21	US-10-775-180-417 Sequence 417, Ap
63	74	47.7	180	21	US-10-775-180-418 Sequence 418, Ap
64	74	47.7	180	21	US-10-775-180-419 Sequence 419, Ap
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66	74	47.7	180	21	US-10-775-180-421 Sequence 421, Ap
67	74	47.7	180	21	US-10-775-180-422 Sequence 422, Ap
68	74	47.7	180	21	US-10-775-180-423 Sequence 423, Ap
69	74	47.7	180	21	US-10-775-180-424 Sequence 424, Ap
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74	74	47.7	180	21	US-10-775-180-429 Sequence 429, Ap
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80	74	47.7	180	21	US-10-775-180-435 Sequence 435, Ap
81	74	47.7	180	21	US-10-775-180-436 Sequence 436, Ap
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83	74	47.7	180	21	US-10-775-180-438 Sequence 438, Ap
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90	74	47.7	180	21	US-10-775-180-445 Sequence 445, Ap
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92	74	47.7	180	21	US-10-775-180-447 Sequence 447, Ap
93	74	47.7	180	21	US-10-775-180-448 Sequence 448, Ap
94	74	47.7	180	21	US-10-775-180-449 Sequence 449, Ap
95	74	47.7	180	21	US-10-775-180-450 Sequence 450, Ap
96	74	47.7	180	21	US-10-775-180-451 Sequence 451, Ap
97	74	47.7	180	21	US-10-775-180-452 Sequence 452, Ap
98	74	47.7	180	21	US-10-775-180-453 Sequence 453, Ap
99	74	47.7	180	21	US-10-775-180-454 Sequence 454, Ap
100	74	47.7	180	21	US-10-775-180-455 Sequence 455, Ap

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 16, 2005, 20:52:27 ; Search time 123.5 Seconds

(without alignments)
490.221 Million cell updates/sec

Title: "us-10-042-746-1"

Perfect score: 155
Sequence: 1 XXHADGSPSBMTXLDXLLAXXDFINWLLXXTKITDXX 37

Scoring table:

BLOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Command line parameters:

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-DB=Issued_Patents_NA -QFMT=faasap -SUFFIX=nti -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62DX -TRANS=human40.cdi
-LIST=200 -DOCLIN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=200
-MOD=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US10042726 @CGN 1.1 93 @runat_14102005_180154_4144 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESDTRY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEF_TIMEOUT=120 -MARK_TIMEOUT=30 -THRAID=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	155	100.0	895 3	US-08-784-582-55 Sequence 55, Appl
2	155	100.0	955 3	US-08-784-582-57 Sequence 57, Appl
3	155	100.0	955 3	US-08-784-582-60 Sequence 60, Appl
4	155	100.0	1062 4	US-09-016-434-1212 Sequence 1212, Ap
5	155	100.0	2356 3	US-08-784-582-72 Sequence 72, Appl
6	79	51.0	207 1	US-08-193-863-3 Sequence 3, Appl
7	79	51.0	207 1	US-08-377-833-3 Sequence 3, Appl
8	79	51.0	207 1	US-08-324-502-3 Sequence 3, Appl
9	79	51.0	207 1	US-08-083-501-3 Sequence 3, Appl
10	79	51.0	207 1	US-08-415-933-3 Sequence 3, Appl
11	76	49.0	143 2	US-08-835-231-14 Sequence 14, Appl
12	76	49.0	143 3	US-09-108-661-14 Sequence 14, Appl

13	76	49.0	159 2	US-08-835-231-15 Sequence 15, Appl
14	76	49.0	159 3	US-09-108-661-15 Sequence 15, Appl
15	76	49.0	711 4	US-09-949-016-3581 Sequence 3581, Ap
16	76	49.0	13795 4	US-09-949-016-15323 Sequence 15323, A
17	74	47.7	110 1	US-07-741-931-8 Sequence 8, Appl
18	74	47.7	110 1	US-07-741-931-9 Sequence 9, Appl
19	74	47.7	110 1	US-07-937-132A-9 Sequence 9, Appl
20	74	47.7	110 1	US-07-937-132A-8 Sequence 8, Appl
21	74	47.7	110 1	US-07-937-132A-9 Sequence 9, Appl
22	74	47.7	144 2	US-08-835-231-17 Sequence 17, Appl
23	74	47.7	144 3	US-09-108-661-17 Sequence 17, Appl
24	74	47.7	255 4	US-09-280-030-51 Sequence 51, Appl
25	74	47.7	561 2	US-08-835-231-3 Sequence 3, Appl
26	74	47.7	561 3	US-08-835-231-4 Sequence 4, Appl
27	74	47.7	561 3	US-09-108-661-3 Sequence 3, Appl
28	74	47.7	561 3	US-09-108-661-4 Sequence 4, Appl
29	72	46.5	87 1	US-07-741-931-1 Sequence 1, Appl
30	72	46.5	87 4	US-07-937-132A-1 Sequence 1, Appl
31	72	46.5	87 4	US-09-280-030-59 Sequence 59, Appl
32	72	46.5	528 2	US-08-835-231-7 Sequence 7, Appl
33	72	46.5	528 2	US-08-835-231-8 Sequence 8, Appl
34	72	46.5	528 3	US-09-108-661-7 Sequence 7, Appl
35	69	44.5	107 1	US-07-741-931-11 Sequence 11, Appl
36	69	44.5	107 1	US-07-937-132A-11 Sequence 11, Appl
37	66	42.6	107 1	US-07-741-931-10 Sequence 10, Appl
38	66	42.6	107 1	US-07-937-132A-10 Sequence 10, Appl
39	62	40.0	492 4	US-09-019-172-1 Sequence 1, Appl
40	61	39.4	138 4	US-09-614-847-146 Sequence 146, App
41	61	39.4	3784 1	US-07-623-033-1 Sequence 1, Appl
42	60	38.7	61847 4	US-09-949-016-16677 Sequence 16677, A
43	59	38.1	1477 4	US-09-949-016-1684 Sequence 1684, Ap
44	59	38.1	1511 4	US-09-708-392-16 Sequence 16, Appl
45	59	38.1	1511 4	US-09-708-392-18 Sequence 18, Appl
46	59	38.1	1511 4	US-09-708-392-16 Sequence 16, Appl
47	58.5	37.7	344 4	US-09-949-016-481 Sequence 1481, App
48	58.5	37.7	1826 3	US-09-270-767-16646 Sequence 16646, A
49	58.5	37.7	1826 3	US-09-286-991-11 Sequence 11, Appl
50	58.5	37.7	1826 3	US-09-687-147-11 Sequence 11, Appl
51	57.5	37.1	16561 4	US-09-949-016-13032 Sequence 13032, A
52	57	36.8	1106 3	US-08-755-587-18 Sequence 18, Appl
53	57	36.8	2184 3	US-08-755-587-170 Sequence 170, App
54	57	36.8	5860 4	US-09-949-016-4463 Sequence 4463, Ap
55	57	36.8	6944 4	US-09-949-016-3637 Sequence 3637, Ap
56	56.5	36.5	1308 4	US-09-134-000C-1087 Sequence 1087, Ap
57	56	36.1	366 3	US-08-908-643C-54 Sequence 54, Appl
58	56	36.1	426 3	US-08-908-643C-52 Sequence 52, Appl
59	56	36.1	498 3	US-08-908-643C-50 Sequence 50, Appl
60	56	36.1	702 3	US-08-887-534A-15 Sequence 15, Appl
61	56	36.1	702 4	US-08-887-534A-15 Sequence 15, Appl
62	56	36.1	702 4	US-09-527-431-15 Sequence 15, Appl
63	56	36.1	1079 3	US-09-446-861-15 Sequence 15, Appl
64	56	36.1	1079 3	US-08-789-329C-2 Sequence 2, Appl
65	56	36.1	1471 3	US-08-887-534A-17 Sequence 17, Appl
66	56	36.1	1471 3	US-08-887-534A-19 Sequence 19, Appl
67	56	36.1	1471 4	US-09-527-431-17 Sequence 17, Appl
68	56	36.1	1471 4	US-09-527-431-19 Sequence 19, Appl
69	56	36.1	1471 4	US-09-446-861-17 Sequence 17, Appl
70	56	36.1	1471 4	US-09-446-861-19 Sequence 19, Appl
71	56	36.1	1636 3	US-08-908-643C-1 Sequence 1, Appl
72	56	36.1	3602 3	US-08-908-643C-85 Sequence 85, Appl
73	56	36.1	3745 3	US-08-908-643C-84 Sequence 84, Appl
74	56	36.1	6022 4	US-08-956-1718-92 Sequence 92, Appl
75	56	36.1	6022 4	US-08-781-986A-92 Sequence 92, Appl
76	56	36.1	6529 3	US-08-789-329C-1 Sequence 1, Appl
77	56	36.1	12860 4	US-09-949-016-12223 Sequence 12223, A
78	56	36.1	12861 4	US-09-949-016-12223 Sequence 12223, A
79	56	36.1	79350 4	US-09-949-016-12467 Sequence 12467, A
80	56	36.1	79351 4	US-09-949-016-16275 Sequence 16275, A
81	56	36.1	200663 4	US-09-949-016-12369 Sequence 12369, A
82	56	36.1	203093 4	US-09-949-016-14445 Sequence 14445, A
83	55	35.5	1017 4	US-09-489-039A-2665 Sequence 2665, Ap
84	55	35.5	2538 4	US-09-543-681A-193 Sequence 193, App
85	55	35.5	174170 4	US-09-949-016-14810 Sequence 14810, A

Tue Oct 18 16:18:17 2005

us-10-042-746-1.rng

Page 1

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 17:10:34 ; Search time 373.5 Seconds
(without alignments)

586,427 Million cell updates/sec

Title: US-10-042-746-1
Perfect score: 155
Sequence: 1 XXHADGFSFDEMTXLDLXAXXDFTNWLXKXITDX 37

Scoring table: BLOSUM62DX

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 200 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=x1h
-O=/cgn2.1/USPTO.spool/US10042746/rnat.17102005.100127.4856/app.query.fasta_1.398
-DB=N Geneseq.16Dec04 -OPM=faetap -SUFFIX=ring -MINMATCH=0.1 -LOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62DX -TRANS=human40.cdt
-LIST=200 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=125
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US10042746 -OCGN 1.1.586 -rnat.17102005.100127.4856 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DEEXT=7

Database :

N_Geneseq.16Dec04:*
1: geneseqn19808:*
2: geneseqn19908:*
3: geneseqn20008:*
4: geneseqn20018:*
5: geneseqn20028:*
6: geneseqn20038:*
7: geneseqn20048:*
8: geneseqn20058:*
9: geneseqn20068:*
10: geneseqn20078:*
11: geneseqn20088:*
12: geneseqn20098:*
13: geneseqn20108:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155	100.0	449	6	ABV98066 Human pan
2	155	100.0	449	6	ABV98700 Human pan
3	155	100.0	517	6	ABV98530 Human pan
4	155	100.0	543	10	ADP16132 Human alb
...
...	ADP15896 Human alb

6	155	100.0	543	10	ADP15900	Adf15900 Human alb
7	155	100.0	543	10	ADP16347	Adf16347 Human alb
8	155	100.0	543	10	ADP16130	Adf16130 Human alb
9	155	100.0	543	10	ADP16129	Adf16129 Human alb
10	155	100.0	543	10	ADP16299	Adf16299 Human alb
11	155	100.0	543	10	ADP15899	Adf15899 Human alb
12	155	100.0	543	10	ADP16131	Adf16131 Human alb
13	155	100.0	543	10	ADP16348	Adf16348 Human alb
14	155	100.0	543	10	ADP16133	Adf16133 Human alb
15	155	100.0	543	10	ADP15898	Adf15898 Human alb
16	155	100.0	543	10	ADP16166	Adf16166 Human alb
17	155	100.0	543	10	ADP16170	Adf16170 Human alb
18	155	100.0	543	10	ADP16168	Adf16168 Human alb
19	155	100.0	543	10	ADP16165	Adf16165 Human alb
20	155	100.0	543	10	ADP16172	Adf16172 Human alb
21	155	100.0	543	10	ADP16177	Adf16177 Human alb
22	155	100.0	543	10	ADP16176	Adf16176 Human alb
23	155	100.0	543	10	ADP16172	Adf16172 Human alb
24	155	100.0	543	10	ADP16173	Adf16173 Human alb
25	155	100.0	543	10	ADP16169	Adf16169 Human alb
26	155	100.0	543	10	ADP16171	Adf16171 Human alb
27	155	100.0	543	10	ADP16172	Adf16172 Human alb
28	155	100.0	543	10	ADP16173	Adf16173 Human alb
29	155	100.0	543	10	ADP16174	Adf16174 Human alb
30	155	100.0	543	10	ADP16175	Adf16175 Human alb
31	155	100.0	543	10	ADP16176	Adf16176 Human alb
32	155	100.0	543	10	ADP16177	Adf16177 Human alb
33	155	100.0	543	10	ADP16178	Adf16178 Human alb
34	155	100.0	543	10	ADP16179	Adf16179 Human alb
35	155	100.0	543	10	ADP16180	Adf16180 Human alb
36	155	100.0	543	10	ADP16181	Adf16181 Human alb
37	155	100.0	543	10	ADP16182	Adf16182 Human alb
38	155	100.0	543	10	ADP16183	Adf16183 Human alb
39	155	100.0	543	10	ADP16184	Adf16184 Human alb
40	155	100.0	543	10	ADP16185	Adf16185 Human alb
41	155	100.0	543	10	ADP16186	Adf16186 Human alb
42	155	100.0	543	10	ADP16187	Adf16187 Human alb
43	155	100.0	543	10	ADP16188	Adf16188 Human alb
44	155	100.0	543	10	ADP16189	Adf16189 Human alb
45	155	100.0	543	10	ADP16190	Adf16190 Human alb
46	155	100.0	543	10	ADP16191	Adf16191 Human alb
47	155	100.0	543	10	ADP16192	Adf16192 Human alb
48	155	100.0	543	10	ADP16193	Adf16193 Human alb
49	155	100.0	543	10	ADP16194	Adf16194 Human alb
50	155	100.0	543	10	ADP16195	Adf16195 Human alb
51	155	100.0	543	10	ADP16196	Adf16196 Human alb
52	155	100.0	543	10	ADP16197	Adf16197 Human alb
53	155	100.0	543	10	ADP16198	Adf16198 Human alb
54	155	100.0	543	10	ADP16199	Adf16199 Human alb
55	155	100.0	543	10	ADP16200	Adf16200 Human alb
56	155	100.0	543	10	ADP16201	Adf16201 Human alb
57	155	100.0	543	10	ADP16202	Adf16202 Human alb
58	155	100.0	543	10	ADP16203	Adf16203 Human alb
59	155	100.0	543	10	ADP16204	Adf16204 Human alb
60	155	100.0	543	10	ADP16205	Adf16205 Human alb
61	155	100.0	543	10	ADP16206	Adf16206 Human alb
62	155	100.0	543	10	ADP16207	Adf16207 Human alb
63	155	100.0	543	10	ADP16208	Adf16208 Human alb
64	155	100.0	543	10	ADP16209	Adf16209 Human alb
65	155	100.0	543	10	ADP16210	Adf16210 Human alb
66	155	100.0	543	10	ADP16211	Adf16211 Human alb
67	155	100.0	543	10	ADP16212	Adf16212 Human alb
68	155	100.0	543	10	ADP16213	Adf16213 Human alb
69	155	100.0	543	10	ADP16214	Adf16214 Human alb
70	155	100.0	543	10	ADP16215	Adf16215 Human alb
71	155	100.0	543	10	ADP16216	Adf16216 Human alb
72	155	100.0	543	10	ADP16217	Adf16217 Human alb
73	155	100.0	543	10	ADP16218	Adf16218 Human alb
74	155	100.0	543	10	ADP16219	Adf16219 Human alb
75	155	100.0	543	10	ADP16220	Adf16220 Human alb
76	155	100.0	543	10	ADP16221	Adf16221 Human alb
77	155	100.0	543	10	ADP16222	Adf16222 Human alb
78	155	100.0	543	10	ADP16223	Adf16223 Human alb

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 17:08:30 ; Search time 2836.5 Seconds

(without alignments)
632.062 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155
Sequence: 1 XHHADGSFSDENMTXLDLXKXDFINMLXXTKITDX 37

Scoring table:

BLOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%

Listing first 200 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xjh
-Q=/cgn2.1/USPTO.spool/US10042746/runat.17102005.100127.4844/app.query.fasta.1.398
-DB=GenEmbl -OPMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62DX -TRANS=human40.cdi -LIST=200
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=125 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HSPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USR=US10042746 @CGN.1.1.3851 @runat.17102005.100127.4844 -NCPU=6 -ICPU=3
-NO MMAP -LARGESUBRY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MAIN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELop=6 -DELext=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: *gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_pro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	155	100.0	241 10	AY623893 Phodopus
2	155	100.0	243 10	RATGLUS
3	155	100.0	543 9	BT006813
4	155	100.0	543 12	BT007507

5	155	100.0	574 4	AY242124 Sus acrofi
6	155	100.0	895 6	AR108106 Sequence
7	155	100.0	955 6	AR108107 Sequence
8	155	100.0	955 6	AR108109 Sequence
9	155	100.0	1034 6	A31421 H.sapiens m
10	155	100.0	1036 6	CQ729100 Sequence
11	155	100.0	1053 10	GP1G
12	155	100.0	1062 6	AR270649 Sequence
13	155	100.0	1062 6	HUMGLUC
14	155	100.0	1104 10	OCOGU
15	155	100.0	1108 4	BOVGS
16	155	100.0	1118 10	HAMGG
17	155	100.0	1123 4	AF308439
18	155	100.0	1154 9	BC005278
19	155	100.0	2356 6	AR108119
20	155	100.0	3798 6	CQ493428
21	155	100.0	4146 6	CQ414344
22	155	100.0	6455 6	HSGJUC
23	155	100.0	10050 9	HSGJUC2
24	155	100.0	163681 9	AC007750
25	155	100.0	223513 2	AC111919
26	155	100.0	225433 2	AC097841
27	154	99.4	145 6	CQ054796
28	154	99.4	145 6	CQ074034
29	154	99.4	145 6	CQ104933
30	154	99.4	145 6	CQ143637
31	154	99.4	145 6	CQ179117
32	154	99.4	145 6	CQ203473
33	154	99.4	145 6	CQ226837
34	154	99.4	145 6	CQ264982
35	154	99.4	145 6	CQ302070
36	154	99.4	145 6	CQ339262
37	150	96.8	668 10	MBPBDGLG
38	150	96.8	1102 10	BC012975
39	150	96.8	1116 10	AF276754
40	150	96.8	188169 10	AL9288576
41	150	96.8	209762 2	AC115074
42	150	96.8	219014 2	AC024141
43	142	91.6	559 4	AX147453
44	142	91.6	1056 6	AX147453
45	109	70.3	1186 5	B78477
46	109	70.3	1360 5	BC075391
47	105	67.7	360 6	CQ049765
48	105	67.7	360 6	CQ064797
49	105	67.7	360 6	CQ091744
50	105	67.7	360 6	CQ130570
51	105	67.7	360 6	CQ169179
52	105	67.7	360 6	CQ198311
53	105	67.7	360 6	CQ213772
54	105	67.7	360 6	CQ252355
55	105	67.7	360 6	CQ289502
56	105	67.7	360 6	CQ326482
57	103	66.5	1408 5	AF004432
58	102	65.8	732 5	AY485817
59	101	65.2	892 5	AY485820
60	101	65.2	1050 5	HSU77612
61	97	62.6	984 5	AY485816
62	96	61.9	790 5	AY485819
63	96	61.9	1300 5	AF324209
64	93	60.0	796 5	AF159707
65	91	58.7	738 5	AF159708
66	91	58.7	974 5	AY485815
67	88	56.8	1014 5	OMU19914
68	88	56.8	1041 5	OMU19917
69	88	56.8	1041 5	S78475
70	85	54.8	1045 5	AY485809
71	85	54.8	1045 5	AY485812
72	85	54.8	2491 5	AY485821
73	84	54.2	520 5	AY485818
74	83	53.5	383 5	OMU19913
75	83	53.5	383 5	OMU19920
76	83	53.5	400 5	OTU19920
77	83	53.5	400 5	S78473
				S78474

AY242124 Sus acrofi	AY242124 Sus acrofi
AR108106 Sequence	AR108106 Sequence
AR108107 Sequence	AR108107 Sequence
AR108109 Sequence	AR108109 Sequence
A31421 H.sapiens m	A31421 H.sapiens m
CQ729100 Sequence	CQ729100 Sequence
D00014 Cavia porce	D00014 Cavia porce
AR270649 Sequence	AR270649 Sequence
J04040 Human gluc	J04040 Human gluc
M57688 Octodon deg	M57688 Octodon deg
K00107 Bovine panc	K00107 Bovine panc
J00059 Syrian hams	J00059 Syrian hams
AF308439 Cavia fam	AF308439 Cavia fam
BC005278 Homo sapi	BC005278 Homo sapi
AR108119 Sequence	AR108119 Sequence
CQ493428 Sequence	CQ493428 Sequence
CQ414344 Sequence	CQ414344 Sequence
V01515 Human gene	V01515 Human gene
X03991 Human gluc	X03991 Human gluc
AC007750 Homo sapi	AC007750 Homo sapi
AC111919 Rattus no	AC111919 Rattus no
AC097841 Rattus no	AC097841 Rattus no
CQ054796 Sequence	CQ054796 Sequence
CQ074034 Sequence	CQ074034 Sequence
CQ104933 Sequence	CQ104933 Sequence
CQ143637 Sequence	CQ143637 Sequence
CQ179117 Sequence	CQ179117 Sequence
CQ203473 Sequence	CQ203473 Sequence
CQ226837 Sequence	CQ226837 Sequence
CQ264982 Sequence	CQ264982 Sequence
CQ302070 Sequence	CQ302070 Sequence
CQ339262 Sequence	CQ339262 Sequence
Z46845 M.musculus	Z46845 M.musculus
BC012975 Mus muscu	BC012975 Mus muscu
AF276754 Mus muscu	AF276754 Mus muscu
AL9288576 Mouse DNA	AL9288576 Mouse DNA
AC024141 Mus muscu	AC024141 Mus muscu
AF529185 Ovis arie	AF529185 Ovis arie
AX147453 Sequence	AX147453 Sequence
S78477 proglucagon	S78477 proglucagon
BC075391 Xenopus t	BC075391 Xenopus t
CQ049765 Sequence	CQ049765 Sequence
CQ064797 Sequence	CQ064797 Sequence
CQ091744 Sequence	CQ091744 Sequence
CQ130570 Sequence	CQ130570 Sequence
CQ169179 Sequence	CQ169179 Sequence
CQ198311 Sequence	CQ198311 Sequence
CQ213772 Sequence	CQ213772 Sequence
CQ252355 Sequence	CQ252355 Sequence
CQ289502 Sequence	CQ289502 Sequence
CQ326482 Sequence	CQ326482 Sequence
AF004432 Xenopus l	AF004432 Xenopus l
AY485817 Squalus a	AY485817 Squalus a
AY485820 Agkistrod	AY485820 Agkistrod
U77612 Heloderma s	U77612 Heloderma s
AY485816 Neocerato	AY485816 Neocerato
AY485819 Bufo mari	AY485819 Bufo mari
AF324209 Hoplobatr	AF324209 Hoplobatr
AF159707 Petromyzo	AF159707 Petromyzo
AF159708 Petromyzo	AF159708 Petromyzo
AY485815 Proctoper	AY485815 Proctoper
U9914 Oncothychnu	U9914 Oncothychnu
U9917 Oncothychnu	U9917 Oncothychnu
S78475 proglucagon	S78475 proglucagon
AY485809 Sebastes	AY485809 Sebastes
AY485821 Ictalurus	AY485821 Ictalurus
AY485818 Hydrolagu	AY485818 Hydrolagu
U19913 Oncothychnu	U19913 Oncothychnu
U19920 Oncothychnu	U19920 Oncothychnu
S78473 Oncothychnu	S78473 Oncothychnu
S78474 proglucagon	S78474 proglucagon

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 16:34:36 ; Search time 2275 Seconds
(without alignments)
619.067 Million cell updates/sec

Title: US-10-042-746-1
Perfect score: 155
Sequence: 1 XHHADGSPSDEMTXLDLAXXDFINMLXTTIDXX 37

Scoring table: BLOSUM62X
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-O/cq22_1/USPTO.spool/US10042746/runat.17102005.100049.4729/app.query.fasta.1.398
-DB=EST -OPMT=fastap -SUFFIX=est -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-INITs=bits -START=1 -END=1 -MATRIX=blomsum62X -TRANS=human40.cdi -LIST=500
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=250 -MODE=LOCAL
-OUTFMT=pct -NORH=ext -HEAPSZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10042746 -CCN=1.4385 -@runat.17102005.100049.4729 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NMG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST :
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_g981.*
9: gb_g982.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	155	100.0	224	5	BU951728
2	155	100.0	310	5	BU074812
3	155	100.0	340	5	BU785759
4	155	100.0	378	5	BU949819
5	155	100.0	384	6	CB178364
6	155	100.0	389	5	BO632756
7	155	100.0	391	6	CA777022
8	155	100.0	400	6	CB068992
9	155	100.0	401	6	CA949891

10	155	100.0	403	6	CA946915
11	155	100.0	409	6	CB070384
12	155	100.0	419	6	EM836042
13	155	100.0	420	5	BQ786903
14	155	100.0	421	7	CK822370
15	155	100.0	425	6	CB178016
16	155	100.0	428	5	BQ271407
17	155	100.0	431	5	BO632726
18	155	100.0	434	5	BM352677
19	155	100.0	435	5	BU074878
20	155	100.0	439	5	BU077375
21	155	100.0	441	6	CA842357
22	155	100.0	442	2	AM190333
23	155	100.0	443	2	CA865479
24	155	100.0	445	6	BO788028
25	155	100.0	446	6	CA843073
26	155	100.0	450	6	CA948774
27	155	100.0	451	6	BM503895
28	155	100.0	451	4	BO776591
29	155	100.0	451	5	CB067109
30	155	100.0	452	6	AM243578
31	155	100.0	454	2	BU078231
32	155	100.0	454	5	BU948794
33	155	100.0	464	5	CB178614
34	155	100.0	464	6	CA848770
35	155	100.0	466	6	CB069084
36	155	100.0	466	6	CB069665
37	155	100.0	469	6	BI791800
38	155	100.0	470	4	BM505325
39	155	100.0	471	4	CA948241
40	155	100.0	471	6	BM12561
41	155	100.0	473	4	BI439035
42	155	100.0	474	4	BI467273
43	155	100.0	474	4	CA777299
44	155	100.0	475	5	BU786347
45	155	100.0	478	5	BM12257
46	155	100.0	479	4	CBM12257
47	155	100.0	479	6	CBM12257
48	155	100.0	482	7	CBM12257
49	155	100.0	482	7	CBM12257
50	155	100.0	487	5	BM122448
51	155	100.0	488	5	BM786347
52	155	100.0	488	6	CA841163
53	155	100.0	490	4	BM509838
54	155	100.0	492	5	BU952083
55	155	100.0	492	6	CA772727
56	155	100.0	494	6	BI791789
57	155	100.0	495	5	BQ271348
58	155	100.0	496	5	BI712848
59	155	100.0	496	4	BI438781
60	155	100.0	498	4	CB069518
61	155	100.0	499	6	CA948911
62	155	100.0	499	6	CA950017
63	155	100.0	501	4	BI712915
64	155	100.0	501	6	CA941615
65	155	100.0	504	4	BM504973
66	155	100.0	506	4	BG655424
67	155	100.0	507	5	BU949129
68	155	100.0	508	4	BG655984
69	155	100.0	508	6	BU072728
70	155	100.0	509	4	CA776542
71	155	100.0	509	4	BI715338
72	155	100.0	511	5	BM150506
73	155	100.0	512	6	BQ632620
74	155	100.0	513	5	BU950509
75	155	100.0	515	6	CA867509
76	155	100.0	516	6	CA952216
77	155	100.0	516	6	CA777150
78	155	100.0	519	6	CB067101
79	155	100.0	521	4	BM311172
80	155	100.0	522	6	BG654407
81	155	100.0	522	6	CA842549
82	155	100.0	522	6	CA943101

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CB067109	1q32B10.y
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BU948794	1m72h06.x
CB178614	1e37E01.x
CB069084	1i25C05.y
CB069665	1826E05.x
BI791800	1e04Q03.y
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CA948241	1q19Q03.y
BM12561	1976B07.y
BI439035	1c25G02.y
BI467273	1c22C02.x
CA777299	1P05H04.y
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BM509838	1994E02.y
BU952083	1m73D05.y
CA772727	1o84B04.y
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BQ271348	1K12E12.y
BI712848	1d98E01.y
BI438781	1c26E01.x
CB069518	1816C04.y
CA948911	1d29G09.y
CA950017	1i85F08.y
BI712915	1d98I02.y
CA941615	1i73E10.y
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CA776542	1P06E03.y
BI715338	1c31E04.y
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CA848560	1P36C02.y
BU950509	1o78C02.y
CA867509	1i29C03.y
CA952216	1d16E09.y
CA777150	1p03E06.y
CB067101	1832E02.y
BM311172	1832E02.y
BG654407	1832E02.y
CA842549	1832E02.y
CA943101	1832E02.y

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OM protein - protein search, using sw model

Run on: October 17, 2005, 15:17:48 ; Search time 54.5 Seconds

(without alignments)
282.986 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155
Sequence: 1 XHHADGSPDEMTYLDLXAXDFINWXXITDX 37

Scoring table: BLOSUM62GX
Gapop 10.0 , Gapext 0.5

Searched: 1860064 seqs, 416830855 residues

Total number of hits satisfying chosen parameters: 1860064

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 200 summaries

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	155	100.0	37	15	US-10-393-524A-4
5	155	100.0	37	15	US-10-393-524A-5
6	155	100.0	37	15	US-10-393-524A-11
7	155	100.0	180	16	US-10-793-677-1
8	155	100.0	180	17	US-10-775-180-198
9	155	100.0	180	17	US-10-775-180-199
10	155	100.0	180	17	US-10-775-180-200
11	155	100.0	180	17	US-10-775-180-201

12	155	100.0	180	17	US-10-775-180-426	Sequence 426, App
13	155	100.0	180	17	US-10-775-180-427	Sequence 427, App
14	155	100.0	180	17	US-10-775-180-428	Sequence 428, App
15	155	100.0	180	17	US-10-775-180-429	Sequence 429, App
16	155	100.0	180	17	US-10-775-180-430	Sequence 430, App
17	155	100.0	180	17	US-10-775-180-651	Sequence 651, App
18	155	100.0	180	17	US-10-775-180-675	Sequence 675, App
19	155	100.0	180	17	US-10-775-180-676	Sequence 676, App
20	155	100.0	180	17	US-10-871-709-2	Sequence 2, Appl
21	155	100.0	180	18	US-10-775-204-630	Sequence 630, App
22	155	100.0	180	18	US-10-775-204-632	Sequence 632, App
23	155	100.0	180	18	US-10-775-204-633	Sequence 633, App
24	155	100.0	180	18	US-10-775-204-634	Sequence 634, App
25	155	100.0	180	18	US-10-775-204-1246	Sequence 1246, App
26	155	100.0	180	18	US-10-775-204-1247	Sequence 1247, App
27	155	100.0	180	18	US-10-775-204-1248	Sequence 1248, App
28	155	100.0	180	18	US-10-775-204-1249	Sequence 1249, App
29	155	100.0	180	18	US-10-775-204-1250	Sequence 1250, App
30	155	100.0	180	18	US-10-775-204-1727	Sequence 1727, App
31	155	100.0	180	18	US-10-775-204-1775	Sequence 1775, App
32	155	100.0	180	18	US-10-775-204-1776	Sequence 1776, App
33	153	98.7	180	20	US-11-060-291-4	Sequence 4, Appl
34	153	98.7	47	9	US-09-864-761-13848	Sequence 33848, A
35	152	98.1	34	16	US-10-203-808-5	Sequence 5, Appl
36	152	98.1	34	16	US-10-203-808-15	Sequence 15, Appl
37	152	98.1	34	16	US-10-737-290-175	Sequence 175, App
38	152	98.1	34	20	US-11-066-697-346	Sequence 346, App
39	152	98.1	78	15	US-10-424-599-172728	Sequence 172728
40	151	97.4	33	14	US-10-295-820-1	Sequence 1, Appl
41	151	97.4	33	14	US-10-042-746-3	Sequence 3, Appl
42	151	97.4	33	14	US-10-042-746-4	Sequence 4, Appl
43	151	97.4	33	14	US-10-293-941-2	Sequence 2, Appl
44	151	97.4	33	15	US-10-201-888-30	Sequence 30, Appl
45	151	97.4	33	15	US-10-393-524A-3	Sequence 3, Appl
46	151	97.4	33	15	US-10-393-524A-13	Sequence 13, Appl
47	151	97.4	33	15	US-10-393-524A-12	Sequence 12, Appl
48	151	97.4	33	16	US-10-685-568-1	Sequence 1, Appl
49	151	97.4	33	16	US-10-730-215-6	Sequence 6, Appl
50	151	97.4	33	16	US-10-730-215-7	Sequence 7, Appl
51	151	97.4	33	16	US-10-203-808-1	Sequence 1, Appl
52	151	97.4	33	16	US-10-203-808-3	Sequence 3, Appl
53	151	97.4	33	16	US-10-203-808-4	Sequence 4, Appl
54	151	97.4	33	16	US-10-203-808-6	Sequence 6, Appl
55	151	97.4	33	16	US-10-203-808-16	Sequence 16, Appl
56	151	97.4	33	16	US-10-203-808-14	Sequence 14, Appl
57	151	97.4	33	16	US-10-203-808-15	Sequence 15, Appl
58	151	97.4	33	17	US-10-847-220-3	Sequence 24, Appl
59	151	97.4	33	17	US-10-919-325-31	Sequence 31, Appl
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61	151	97.4	45	18	US-10-993-127-4	Sequence 4, Appl
62	151	97.4	34	16	US-10-203-808-10	Sequence 2, Appl
63	148	95.5	34	16	US-10-203-808-12	Sequence 12, Appl
64	148	95.5	34	16	US-10-203-808-23	Sequence 23, Appl
65	148	95.5	34	16	US-10-203-808-18	Sequence 18, Appl
66	147	94.8	33	16	US-10-393-524A-14	Sequence 14, Appl
67	147	94.8	33	16	US-10-203-808-7	Sequence 7, Appl
68	147	94.8	33	16	US-10-203-808-8	Sequence 8, Appl
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71	147	94.8	33	16	US-10-203-808-13	Sequence 13, Appl
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73	145	93.5	33	16	US-10-203-808-17	Sequence 17, Appl
74	145	93.5	33	16	US-10-203-808-18	Sequence 18, Appl
75	145	93.5	33	16	US-10-203-808-20	Sequence 20, Appl
76	145	93.5	33	16	US-10-203-808-21	Sequence 21, Appl
77	145	93.5	33	16	US-10-203-808-26	Sequence 26, Appl
78	145	93.5	33	16	US-10-203-808-27	Sequence 27, Appl
79	145	93.5	33	16	US-10-997-078-35	Sequence 35, Appl
80	144	92.9	33	16	US-10-203-808-19	Sequence 19, Appl
81	144	92.9	33	16	US-10-203-808-22	Sequence 22, Appl
82	144	92.9	33	16	US-10-203-808-28	Sequence 28, Appl
83	144	92.9	33	16	US-10-997-078-36	Sequence 36, Appl
84	141	91.0	34	18	US-10-997-078-38	Sequence 38, Appl

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OM protein - protein search, using sw model

Run on: October 16, 2005, 14:54:46 ; Search time 52.5 Seconds
(without alignments)

52.610 Million cell updates/sec

Title: US-10-042-746-1

Sequence: 1 XXHADGSPDEMTXLDLXXDFIWMXXITTDXX 37

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	155	100.0	37	2	US-08-422-540A-4
6	155	100.0	37	2	US-08-422-540A-5
7	155	100.0	37	2	US-08-422-540A-6
8	155	100.0	37	2	US-08-422-540A-7
9	155	100.0	37	2	US-08-784-582-56
10	155	100.0	180	3	US-08-784-582-58
11	155	100.0	180	3	US-08-784-582-61
12	155	100.0	360	3	US-08-784-582-73
13	153	98.7	48	2	US-08-808-825-8
14	151	97.4	33	1	US-08-669-791C-2
15	151	97.4	33	2	US-08-669-790C-3
16	151	97.4	33	2	US-08-669-790C-4
17	151	97.4	33	2	US-08-808-825-5
18	151	97.4	33	2	US-08-808-825-6
19	151	97.4	33	2	US-08-808-825-7
20	151	97.4	33	2	US-08-422-540A-3
21	151	97.4	33	3	US-08-835-538C-2
22	151	97.4	33	3	US-09-149-831-1
23	151	97.4	33	3	US-09-149-831-2
24	151	97.4	33	4	US-09-233-934-1
25	151	97.4	33	4	US-09-692-238-1
26	151	97.4	33	4	US-09-692-238-2
27	147	94.8	33	1	US-08-669-791C-5

28	140	90.3	35	2	US-08-808-825-1	Sequence 1, Appl
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30	79	51.0	69	1	US-08-193-863-1	Sequence 1, Appl
31	79	51.0	69	1	US-08-377-833-1	Sequence 1, Appl
32	79	51.0	69	1	US-08-324-502-1	Sequence 1, Appl
33	79	51.0	69	1	US-08-083-501-1	Sequence 1, Appl
34	79	51.0	69	1	US-08-415-939-1	Sequence 1, Appl
35	79	51.0	69	1	US-08-548-152-1	Sequence 1, Appl
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37	79	51.0	70	1	US-08-377-833-2	Sequence 2, Appl
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41	79	51.0	70	1	US-08-548-152-2	Sequence 2, Appl
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43	77	49.7	39	3	US-09-258-750-91	Sequence 91, Appl
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74	75	48.4	34	4	US-09-398-111-13	Sequence 13, Appl
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76	75	48.4	187	2	US-08-835-231-16	Sequence 16, Appl
77	75	48.4	187	2	US-09-108-661-16	Sequence 16, Appl
78	74	47.7	29	4	US-09-847-249A-72	Sequence 72, Appl
79	74	47.7	34	1	US-08-095-162-6	Sequence 6, Appl
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81	74	47.7	34	3	US-08-967-374-6	Sequence 6, Appl
82	74	47.7	34	3	US-08-258-750-66	Sequence 66, Appl
83	74	47.7	34	4	US-09-505-991-6	Sequence 6, Appl
84	74	47.7	34	4	US-09-398-111-66	Sequence 66, Appl
85	74	47.7	34	4	US-09-212-663-25	Sequence 25, Appl
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87	74	47.7	35	3	US-09-258-750-58	Sequence 58, Appl
88	74	47.7	35	3	US-09-258-750-67	Sequence 67, Appl
89	74	47.7	35	4	US-09-398-111-58	Sequence 58, Appl
90	74	47.7	35	4	US-09-398-111-67	Sequence 67, Appl
91	74	47.7	36	1	US-08-095-162-15	Sequence 15, Appl
92	74	47.7	36	1	US-08-470-220A-15	Sequence 15, Appl
93	74	47.7	36	2	US-08-808-825-9	Sequence 9, Appl
94	74	47.7	36	2	US-08-899-324-1	Sequence 1, Appl
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96	74	47.7	36	3	US-08-399-892B-1	Sequence 1, Appl
97	74	47.7	36	3	US-09-258-750-59	Sequence 59, Appl
98	74	47.7	36	3	US-09-258-750-68	Sequence 68, Appl
99	74	47.7	36	3	US-09-302-996-2	Sequence 2, Appl
100	74	47.7	36	3	US-09-302-996-2	Sequence 2, Appl

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OM protein - protein search, using sw model

Run on: October 17, 2005, 12:43:07 ; Search time 56 Seconds

(without alignments)
255,538 Million cell updates/sec

Title: US-10-042-746-1

Sequence: 1 XXHADGFSFDEMTXLDXAXXDPIWXXXTITDX 37

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 200 summaries

Database : A_Geneseq.16Dec04:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	155	100.0	180	2	AAW22081 Human pre
6	155	100.0	180	2	AAW22079 Rat prepr
7	155	100.0	180	2	AAW22080 Human pre
8	155	100.0	180	3	AAW39812 Preproglu
9	155	100.0	180	3	AAW39812 Preproglu
10	155	100.0	180	3	AAW39812 Preproglu
11	155	100.0	180	3	AAW39812 Preproglu
12	155	100.0	180	3	AAW39812 Preproglu
13	155	100.0	180	3	AAW39812 Preproglu
14	155	100.0	180	3	AAW39812 Preproglu
15	155	100.0	180	3	AAW39812 Preproglu
16	155	100.0	180	3	AAW39812 Preproglu
17	155	100.0	180	3	AAW39812 Preproglu
18	155	100.0	180	3	AAW39812 Preproglu
19	155	100.0	180	3	AAW39812 Preproglu
20	155	100.0	180	3	AAW39812 Preproglu
21	155	100.0	180	3	AAW39812 Preproglu
22	155	100.0	180	3	AAW39812 Preproglu
23	155	100.0	180	3	AAW39812 Preproglu
24	155	100.0	180	3	AAW39812 Preproglu
25	155	100.0	180	3	AAW39812 Preproglu

26	155	100.0	180	7	ADH21633 Human GLP
27	155	100.0	180	7	ADH21633 Human GLP
28	155	100.0	180	7	ADH21633 Human GLP
29	155	100.0	180	7	ADH21633 Human GLP
30	155	100.0	180	7	ADH21633 Human GLP
31	155	100.0	180	7	ADH21633 Human GLP
32	155	100.0	180	7	ADH21633 Human GLP
33	155	100.0	180	7	ADH21633 Human GLP
34	155	100.0	180	7	ADH21633 Human GLP
35	155	100.0	180	7	ADH21633 Human GLP
36	155	100.0	180	7	ADH21633 Human GLP
37	155	100.0	180	7	ADH21633 Human GLP
38	155	100.0	180	7	ADH21633 Human GLP
39	155	100.0	180	7	ADH21633 Human GLP
40	155	100.0	180	7	ADH21633 Human GLP
41	155	100.0	180	7	ADH21633 Human GLP
42	155	100.0	180	7	ADH21633 Human GLP
43	155	100.0	180	7	ADH21633 Human GLP
44	155	100.0	180	7	ADH21633 Human GLP
45	155	100.0	180	7	ADH21633 Human GLP
46	155	100.0	180	7	ADH21633 Human GLP
47	155	100.0	180	7	ADH21633 Human GLP
48	155	100.0	180	7	ADH21633 Human GLP
49	155	100.0	180	7	ADH21633 Human GLP
50	155	100.0	180	7	ADH21633 Human GLP
51	155	100.0	180	7	ADH21633 Human GLP
52	155	100.0	180	7	ADH21633 Human GLP
53	155	100.0	180	7	ADH21633 Human GLP
54	155	100.0	180	7	ADH21633 Human GLP
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57	155	100.0	180	7	ADH21633 Human GLP
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64	155	100.0	180	7	ADH21633 Human GLP
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66	155	100.0	180	7	ADH21633 Human GLP
67	155	100.0	180	7	ADH21633 Human GLP
68	155	100.0	180	7	ADH21633 Human GLP
69	155	100.0	180	7	ADH21633 Human GLP
70	155	100.0	180	7	ADH21633 Human GLP
71	155	100.0	180	7	ADH21633 Human GLP
72	155	100.0	180	7	ADH21633 Human GLP
73	155	100.0	180	7	ADH21633 Human GLP
74	155	100.0	180	7	ADH21633 Human GLP
75	155	100.0	180	7	ADH21633 Human GLP
76	155	100.0	180	7	ADH21633 Human GLP
77	155	100.0	180	7	ADH21633 Human GLP
78	155	100.0	180	7	ADH21633 Human GLP
79	155	100.0	180	7	ADH21633 Human GLP
80	155	100.0	180	7	ADH21633 Human GLP
81	155	100.0	180	7	ADH21633 Human GLP
82	155	100.0	180	7	ADH21633 Human GLP
83	155	100.0	180	7	ADH21633 Human GLP
84	155	100.0	180	7	ADH21633 Human GLP
85	155	100.0	180	7	ADH21633 Human GLP
86	155	100.0	180	7	ADH21633 Human GLP
87	155	100.0	180	7	ADH21633 Human GLP
88	155	100.0	180	7	ADH21633 Human GLP
89	155	100.0	180	7	ADH21633 Human GLP
90	155	100.0	180	7	ADH21633 Human GLP
91	155	100.0	180	7	ADH21633 Human GLP
92	155	100.0	180	7	ADH21633 Human GLP
93	155	100.0	180	7	ADH21633 Human GLP
94	155	100.0	180	7	ADH21633 Human GLP
95	155	100.0	180	7	ADH21633 Human GLP
96	155	100.0	180	7	ADH21633 Human GLP
97	155	100.0	180	7	ADH21633 Human GLP
98	155	100.0	180	7	ADH21633 Human GLP

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OM protein - protein search, using sw model

Run on: October 16, 2005, 10:03:46 ; Search time 199.5 Seconds
(without alignments)
94.972 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155

Sequence: 1 XXHADGSEFSDENMTXLDLXAXDFINWLXXTKITDX 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : 1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	155	100.0	061U8	Q61U8 phodopus su
2	155	100.0	GLUC_BOVIN	P01272 b glucagon
3	155	100.0	GLUC_CANFA	P29194 c glucagon
4	155	100.0	GLUC_CANFA	P05110 c glucagon
5	155	100.0	GLUC_CANFA	P01275 h glucagon
6	155	100.0	GLUC_HUMAN	P01273 m glucagon
7	155	100.0	GLUC_MESAU	P22890 o glucagon
8	155	100.0	GLUC_OCTDE	P01274 b glucagon
9	155	100.0	GLUC_PIG	P06883 r glucagon
10	155	100.0	GLUC_RAT	P55095 m glucagon
11	142	91.6	GLUC_MOUSE	P01275 h glucagon
12	109	70.3	GLUC_SHEEP	P01275 h glucagon
13	109	70.3	GLUC_CHICK	P01275 h glucagon
14	103	66.5	GLUC_XENILA	P01275 h glucagon
15	102	65.8	GLUC_XENILA	P01275 h glucagon
16	101	65.2	GLUC_XENILA	P01275 h glucagon
17	101	65.2	GLUC_XENILA	P01275 h glucagon
18	97	62.6	GLUC_XENILA	P01275 h glucagon
19	96	61.9	GLUC_XENILA	P01275 h glucagon
20	96	61.9	GLUC_XENILA	P01275 h glucagon
21	94	60.6	GLUC_XENILA	P01275 h glucagon
22	93	60.6	GLUC_XENILA	P01275 h glucagon
23	91	58.7	GLUC_XENILA	P01275 h glucagon
24	91	58.7	GLUC_XENILA	P01275 h glucagon
25	88	56.8	GLUC_XENILA	P01275 h glucagon
26	88	56.8	GLUC_XENILA	P01275 h glucagon
27	85	54.8	GLUC_XENILA	P01275 h glucagon
28	85	54.8	GLUC_XENILA	P01275 h glucagon
29	85	54.8	GLUC_XENILA	P01275 h glucagon
30	84	54.2	GLUC_XENILA	P01275 h glucagon
31	83	53.5	GLUC_XENILA	P01275 h glucagon

32	83	53.5	72	2	091409	Q91409
33	83	53.5	122	2	06RYB8	Q6RYB8
34	82	52.9	36	1	GLUC_HYDRO	P09682 hydroclase
35	81	52.3	68	1	GLUC_ONCKI	P07449 oncorhynch
36	79	51.0	71	1	GLUC_ICTPU	P04093 ictalurus p
37	79	51.0	122	1	GLUC_LOPAM	P04092 lophus ame
38	79	51.0	219	1	GLUC_XENILA	Q42144 xenopus lae
39	78	50.3	71	1	GLUC_PIRME	P01880 piractus m
40	78	50.3	78	1	GLUC_LBSP	P09566 lepisosteus
41	78	50.3	120	2	06RYB7	Q6RYB7
42	77	49.7	49	7	GLUC_CALMI	P13189 callorhynch
43	77	49.7	62	1	GLUC_SCYA	P09687 scyllorhynch
44	77	49.7	121	1	GLUC_CARAU	P09695 carassius a
45	77	49.7	123	2	06RYA9	Q6RYA9
46	77	49.7	144	1	GIP_RAT	Q6145 ratius norv
47	76	49.0	30	2	07LZN3	Q07123 polyodon sp
48	76	49.0	121	2	06RYC1	Q6RYC1
49	76	49.0	121	2	09DD6	Q09466 brachydantio
50	76	49.0	153	1	GIP_HUMAN	P09681 homo sapien
51	76	49.0	153	2	06NTD3	Q06NTD3 homo sapien
52	75	48.4	42	1	GIP_BOVIN	P09680 bos sapien
53	75	48.4	42	1	GIP_PIG	P01281 sus scrofa
54	74	47.7	29	1	GLUC_TORMA	P09567 torpedo mar
55	74	47.7	36	1	GLUC_ORENI	P01026 oreochromis
56	74	47.7	45	2	06PRF4	Q06PRF4 capra hircu
57	74	47.7	130	2	09CVF1	Q09CVF1 mus musculu
58	74	47.7	144	1	GIP_MOUSE	P048756 mus musculu
59	74	47.7	144	2	09DB87	Q09DB87 mus musculu
60	72	46.5	29	1	GLUC_ANAPL	P01276 anas platyr
61	72	46.5	29	1	GLUC_CAMPD	P08273 camelus dro
62	72	46.5	29	1	GLUC_DIDMA	P01808 didelphis m
63	72	46.5	29	1	GLUC_LAMFL	Q09493 lampetra fi
64	72	46.5	29	1	GLUC_MELGA	P08260 melagris g
65	72	46.5	29	1	GLUC_RABIT	P08274 oryctolagus
66	72	46.5	29	1	GLUC_SAISS	P08275 saimiri sci
67	72	46.5	96	1	GLUC_MYOSC	P09666 myoxocephal
68	72	46.5	124	1	GLUC_LOPAM	P01278 lophus ame
69	72	46.5	500	2	0849N5	Q0849N5 escherichia
70	71	45.8	75	1	GLUC_AMICA	P03528 amia calva
71	70	45.2	29	1	GLUC_PLAFB	P23062 platichthys
72	70	45.2	96	2	09DG43	Q09DG43 anguilla an
73	69	44.5	30	1	GLUC_ANGRO	P03325 anguilla ro
74	69	44.5	29	1	GLUC_CHIBR	P01297 chinchilla
75	67	43.2	87	2	07SZU6	Q07SZU6 heloderma h
76	67	43.2	39	1	EXE3_HELHO	P20334 heloderma h
77	65	41.9	679	2	023352	Q023352 arabidopsis
78	65	41.9	787	2	094C98	Q094C98 arabidopsis
79	65	41.9	31	2	07LZN2	Q07LZN2 polyodon sp
80	63	40.6	928	1	MAY4_SCHCO	P03793 schizophy11
81	62.5	40.3	87	1	EXE4_HELST	P26349 heloderma s
82	62	40.0	387	2	08FSR2	Q08FSR2 corynebacte
83	62	40.0	754	2	08TZO6	Q08TZO6 mus musculu
84	62	40.0	2152	2	09S515	Q09S515 caenorhabdi
85	62	40.0	145	2	07N1M1	Q07N1M1 photorhabdu
86	61.5	39.7	31	2	07LZN4	Q07LZN4 polyodon sp
87	61	39.4	502	2	09R641	Q09R641 deinococcus
88	61	39.4	712	2	09ZRB0	Q09ZRB0 rhabdium m
89	61	39.4	1072	2	HSER_RAT	Q12347 baccharomyc
90	61	39.4	344	2	012347	Q012347 pseudomonas
91	60	38.7	572	2	0882W2	Q0882W2 lactococcus
92	60	38.7	639	2	09CRS3	Q09CRS3 thermomanaer
93	60	38.7	544	2	08RCL2	Q08RCL2 bacteriophag
94	59.5	38.4	94	2	076206	Q076206 macaca fasc
95	59	38.1	145	2	07MXY9	Q07MXY9 macaca fasc
96	59	38.1	170	1	VIP_BOVIN	P01801 bos sapien
97	59	38.1	170	1	VIP_HUMAN	P01282 homo sapien
98	59	38.1	205	2	09T7Z5	Q09T7Z5 oryctolagus
99	59	38.1	295	2	062832	Q062832 bos taurus
100	59	38.1	518	2	038233	Q038233 lactococcus
101	59	38.1	518	2	038233	Q038233 lactococcus
102	59	38.1	1076	1	HSER_CAVPO	P07006 cavia porce
103	59	38.1	1967	2	07RHF3	Q07RHF3 plasmodium
104	59	38.1				

Q91409	oncorhynch
Q6RYB8	ictalurus p
P09682	hydroclase
P07449	oncorhynch
P04093	ictalurus p
P04092	lophus ame
Q42144	xenopus lae
P01880	piractus m
P09566	lepisosteus
Q6RYB7	ictalurus p
P13189	callorhynch
P09687	scyllorhynch
P09695	carassius a
Q6RYA9	sebastes ca
Q06145	ratius norv
Q07123	polyodon sp
Q6RYC1	sebastes ca
Q09466	brachydantio
P09681	homo sapien
Q06NTD3	homo sapien
P09680	bos sapien
P01281	sus scrofa
P09567	torpedo mar
P01026	oreochromis
Q06PRF4	capra hircu
Q09CVF1	mus musculu
P048756	mus musculu
Q09DB87	mus musculu
P01276	anas platyr
P08273	camelus dro
P01808	didelphis m
Q09493	lampetra fi
P08260	melagris g
P08274	oryctolagus
P08275	saimiri sci
P09666	myoxocephal
P01278	lophus ame
Q0849N5	escherichia
P03528	amia calva
P23062	platichthys
Q09DG43	anguilla an
P03325	anguilla ro
P01297	chinchilla
Q07SZU6	heloderma h
P20334	heloderma h
Q023352	arabidopsis
Q094C98	arabidopsis
Q07LZN2	polyodon sp
P03793	schizophy11
P26349	heloderma s
Q08FSR2	corynebacte
Q08TZO6	mus musculu
Q09S515	caenorhabdi
Q07N1M1	photorhabdu
Q07LZN4	polyodon sp
Q09R641	deinococcus
Q09ZRB0	rhabdium m
P01282	homo sapien
Q09T7Z5	oryctolagus
Q062832	bos taurus
Q038233	lactococcus
Q038233	lactococcus
P07006	cavia porce
Q07RHF3	plasmodium

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OM protein - protein search, using sw model

Run on: October 16, 2005, 10:55:31 ; Search time 38.5 Seconds

(without alignments)
92.468 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155
Sequence: 1 XXHADGSFSDENMTXLDLXAXDFINMLXXRTITDX 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155	100.0	180	1	GCXY glucagon precursor
2	155	100.0	180	1	GCYP glucagon precursor
3	155	100.0	180	1	GCYU glucagon precursor
4	155	100.0	180	1	GCRT glucagon precursor
5	155	100.0	180	1	GCRTDU glucagon precursor
6	153	98.7	158	1	GCPR glucagon precursor
7	150	96.8	180	2	GCBO glucagon precursor
8	148	95.5	180	1	GCBO glucagon precursor
9	109	70.3	206	2	151301 glucagon precursor
10	94	60.6	101	1	GCYB glucagon precursor
11	88	56.8	178	2	151057 glucagon precursor
12	88	56.8	178	2	151058 glucagon precursor
13	83	53.5	66	2	151093 glucagon precursor
14	82	52.9	36	1	GCRT glucagon precursor
15	81	52.3	60	1	GCNC glucagon precursor
16	79	51.0	63	1	GCNC glucagon precursor
17	79	51.0	69	1	GCDF glucagon precursor
18	79	51.0	122	1	GCDF glucagon precursor
19	79	51.0	151	1	GCCH glucagon precursor
20	78	50.3	72	1	GCCKA glucagon precursor
21	77	49.7	29	1	GCEN glucagon precursor
22	77	49.7	144	1	UN0589 glucagon precursor
23	76	49.0	30	2	S44473 glucagon precursor
24	76	49.0	153	1	A28406 glucagon precursor
25	75	48.4	42	1	GIBO glucagon precursor
26	75	48.4	42	1	GIBO glucagon precursor
27	74	47.7	29	2	S07211 glucagon precursor
28	74	47.7	144	2	S71426 glucagon precursor
29	72	46.5	29	1	A61583 glucagon precursor

30	72	46.5	29	1	GCDF glucagon precursor
31	72	46.5	29	1	GCDF glucagon precursor
32	72	46.5	29	1	GCDF glucagon precursor
33	72	46.5	29	1	GCDF glucagon precursor
34	72	46.5	29	2	A91740 glucagon precursor
35	72	46.5	29	2	C39258 glucagon precursor
36	72	46.5	29	2	A91742 glucagon precursor
37	72	46.5	29	2	A91741 glucagon precursor
38	72	46.5	87	1	GCPS glucagon precursor
39	72	46.5	124	1	GCAP glucagon precursor
40	71	45.8	29	2	S39018 glucagon precursor
41	70	45.2	29	1	GCFLB glucagon precursor
42	70	45.2	29	2	A61135 glucagon precursor
43	69	44.5	30	2	C61125 glucagon precursor
44	69	44.5	30	2	B61125 glucagon precursor
45	67	43.2	29	1	GCGB glucagon precursor
46	65	41.9	29	2	C60840 glucagon precursor
47	65	41.9	39	1	HMGB32 glucagon precursor
48	65	41.9	679	2	C71413 glucagon precursor
49	63	40.6	31	2	S44472 glucagon precursor
50	62.5	40.3	928	2	C37271 glucagon precursor
51	62	40.0	2172	2	T20145 glucagon precursor
52	61	39.4	31	2	S44471 glucagon precursor
53	61	39.4	502	2	H75290 glucagon precursor
54	61	39.4	1075	1	OYRTHX glucagon precursor
55	60	38.7	39	1	HMGB4G glucagon precursor
56	60	38.7	344	2	S64931 glucagon precursor
57	60	38.7	639	2	A86845 glucagon precursor
58	59	38.1	145	2	A60038 glucagon precursor
59	59	38.1	170	1	VRHU glucagon precursor
60	58	37.4	36	2	D60840 glucagon precursor
61	57.5	37.1	460	2	T39462 glucagon precursor
62	57	36.8	170	1	VRRT glucagon precursor
63	57	36.8	170	1	A60037 glucagon precursor
64	57	36.8	347	2	S56795 glucagon precursor
65	57	36.8	1849	2	T14096 glucagon precursor
66	56.5	36.5	388	2	B69881 glucagon precursor
67	56	36.1	233	2	C89914 glucagon precursor
68	56	36.1	311	2	AH3154 glucagon precursor
69	56	36.1	326	2	A99133 glucagon precursor
70	56	36.1	896	2	S61996 glucagon precursor
71	56	36.1	1073	1	OYRTHX glucagon precursor
72	55.5	35.8	255	2	T38115 glucagon precursor
73	55.5	35.8	365	2	B83952 glucagon precursor
74	55.5	35.8	443	2	T35974 glucagon precursor
75	55.5	35.8	688	2	AH2294 glucagon precursor
76	55.5	35.8	881	2	AE2153 glucagon precursor
77	55	35.5	388	2	H64427 glucagon precursor
78	55	35.5	2054	2	T32413 glucagon precursor
79	54	34.8	920	2	T40863 glucagon precursor
80	54	34.8	920	2	T40771 glucagon precursor
81	54	34.8	968	2	C84452 glucagon precursor
82	54	34.8	1088	2	C83054 glucagon precursor
83	53.5	34.5	254	1	BVY553 glucagon precursor
84	53.5	34.5	606	2	S57552 glucagon precursor
85	53.5	34.5	720	2	T25883 glucagon precursor
86	53.5	34.5	1174	2	AE2911 glucagon precursor
87	53.5	34.5	1174	2	C97686 glucagon precursor
88	53	34.2	320	2	A24815 glucagon precursor
89	53	34.2	325	2	B90764 glucagon precursor
90	53	34.2	330	2	T26317 glucagon precursor
91	53	34.2	349	2	D85678 glucagon precursor
92	53	34.2	349	2	H85626 glucagon precursor
93	53	34.2	349	2	B90819 glucagon precursor
94	53	34.2	380	2	B90912 glucagon precursor
95	53	34.2	380	2	B81302 glucagon precursor
96	53	34.2	414	2	A87165 glucagon precursor
97	53	34.2	490	2	T32057 glucagon precursor
98	53	34.2	571	2	T67737 glucagon precursor
99	53	34.2	714	1	CHUH glucagon precursor
100	52.5	33.9	79	2	AB1982 glucagon precursor
101	52.5	33.9	863	2	B71343 glucagon precursor
102	52	33.5	55	1	VRBB glucagon precursor

glucagon - smaller
glucagon - duck
glucagon - North A
glucagon - slider
glucagon - turkey
glucagon - common
glucagon - Arabian
glucagon - rabbit
glucagon precursor
glucagon I precursor
glucagon - bowfin
glucagon - Europea
glucagon - bigeye
glucagon-like peptide
glucagon-like peptide
glucagon - Chinchi
glucagon I - Burro
exendin-3 - Mexica
hypothetical prote
glucagon G2 - Nort
A-alpha Y 4 protei
hypothetical prote
glucagon G1 - Nort
hypothetical prote
heat-stable entero
exendin-4 - Gila m
hypothetical prote
hypothetical prote
vasoactive intesti
vasoactive intesti
glucagon II - Bur
argininosuccinate
vasoactive intesti
vasoactive intesti
guanine nucleotide
conserved hypothet
hypothetical prote
conserved hypothet
hypothetical prote
hypothetical prote
probable membrane
heat-stable entero
probable AMP-depen
1-deoxy-d-xylose
probable aminoacyl
proteinase II [imp
DNA topoisomerase
hypothetical prote
probable acetyl-Co
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